

Sequence Listing

<110> Baker, Kevin P.  
Botstein, David  
Desnoyers, Luc  
Eaton, Dan L.  
Ferrara, Napoleone  
Fong, Sherman  
Gao, Wei-Qiang  
Goddard, Audrey  
Godowski, Paul J.  
Grimaldi, Christopher J.  
Gurney, Austin L.  
Hillan, Kenneth J.  
Pan, James  
Paoni, Nicholas F.  
Roy, Margaret Ann  
Smith, Victoria  
Stewart, Timothy A.  
Tumas, Daniel  
Watanabe, Colin K.  
Williams, P. Mickey  
Wood, William I.

<120> Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

<130> P2830P1C51

<150> 09/946374  
<151> 2001-09-04

<150> 60/098716  
<151> 1998-09-01

<150> 60/098723  
<151> 1998-09-01

<150> 60/098749  
<151> 1998-09-01

<150> 60/098750  
<151> 1998-09-01

<150> 60/098803  
<151> 1998-09-02

<150> 60/098821  
<151> 1998-09-02

<150> 60/098843  
<151> 1998-09-02

<150> 60/099536  
<151> 1998-09-09

<150> 60/099596  
<151> 1998-09-09

<150> 60/099598  
<151> 1998-09-09

<150> 60/099602  
<151> 1998-09-09

<150> 60/099642  
<151> 1998-09-09

<150> 60/099741  
<151> 1998-09-10

<150> 60/099754  
<151> 1998-09-10

<150> 60/099763  
<151> 1998-09-10

<150> 60/099792  
<151> 1998-09-10

<150> 60/099808  
<151> 1998-09-10

<150> 60/099812  
<151> 1998-09-10

<150> 60/099815  
<151> 1998-09-10

<150> 60/099816  
<151> 1998-09-10

<150> 60/100385  
<151> 1998-09-15

<150> 60/100388  
<151> 1998-09-15

<150> 60/100390  
<151> 1998-09-15

<150> 60/100584  
<151> 1998-09-16

<150> 60/100627  
<151> 1998-09-16

<150> 60/100661  
<151> 1998-09-16

<150> 60/100662  
<151> 1998-09-16

<150> 60/100664  
<151> 1998-09-16

<150> 60/100683

<151> 1998-09-17

<150> 60/100684  
<151> 1998-09-17

<150> 60/100710  
<151> 1998-09-17

<150> 60/100711  
<151> 1998-09-17

<150> 60/100848  
<151> 1998-09-18

<150> 60/100849  
<151> 1998-09-18

<150> 60/100919  
<151> 1998-09-17

<150> 60/100930  
<151> 1998-09-17

<150> 60/101014  
<151> 1998-09-18

<150> 60/101068  
<151> 1998-09-18

<150> 60/101071  
<151> 1998-09-18

<150> 60/101279  
<151> 1998-09-22

<150> 60/101471  
<151> 1998-09-23

<150> 60/101472  
<151> 1998-09-23

<150> 60/101474  
<151> 1998-09-23

<150> 60/101475  
<151> 1998-09-23

<150> 60/101476  
<151> 1998-09-23

<150> 60/101477  
<151> 1998-09-23

<150> 60/101479  
<151> 1998-09-23

<150> 60/101738  
<151> 1998-09-24

<150> 60/101741  
<151> 1998-09-24

<150> 60/101743  
<151> 1998-09-24

<150> 60/101915  
<151> 1998-09-24

<150> 60/101916  
<151> 1998-09-24

<150> 60/102207  
<151> 1998-09-29

<150> 60/102240  
<151> 1998-09-29

<150> 60/102307  
<151> 1998-09-29

<150> 60/102330  
<151> 1998-09-29

<150> 60/102331  
<151> 1998-09-29

<150> 60/102484  
<151> 1998-09-30

<150> 60/102487  
<151> 1998-09-30

<150> 60/102570  
<151> 1998-09-30

<150> 60/102571  
<151> 1998-09-30

<150> 60/102684  
<151> 1998-10-01

<150> 60/102687  
<151> 1998-10-01

<150> 60/102965  
<151> 1998-10-02

<150> 60/103258  
<151> 1998-10-06

<150> 60/103314  
<151> 1998-10-07

<150> 60/103315  
<151> 1998-10-07

<150> 60/103328

<151> 1998-10-07

<150> 60/103395  
<151> 1998-10-07

<150> 60/103396  
<151> 1998-10-07

<150> 60/103401  
<151> 1998-10-07

<150> 60/103449  
<151> 1998-10-06

<150> 60/103633  
<151> 1998-10-08

<150> 60/103678  
<151> 1998-10-08

<150> 60/103679  
<151> 1998-10-08

<150> 60/103711  
<151> 1998-10-08

<150> 60/104257  
<151> 1998-10-14

<150> 60/104987  
<151> 1998-10-20

<150> 60/105000  
<151> 1998-10-20

<150> 60/105002  
<151> 1998-10-20

<150> 60/105104  
<151> 1998-10-21

<150> 60/105169  
<151> 1998-10-22

<150> 60/105266  
<151> 1998-10-22

<150> 60/105693  
<151> 1998-10-26

<150> 60/105694  
<151> 1998-10-26

<150> 60/105807  
<151> 1998-10-27

<150> 60/105881  
<151> 1998-10-27

<150> 60/105882  
<151> 1998-10-27

<150> 60/106023  
<151> 1998-10-28

<150> 60/106029  
<151> 1998-10-28

<150> 60/106030  
<151> 1998-10-28

<150> 60/106032  
<151> 1998-10-28

<150> 60/106033  
<151> 1998-10-28

<150> 60/106062  
<151> 1998-10-27

<150> 60/106178  
<151> 1998-10-28

<150> 60/106248  
<151> 1998-10-29

<150> 60/106384  
<151> 1998-10-29

<150> 60/108500  
<151> 1998-10-29

<150> 60/106464  
<151> 1998-10-30

<150> 60/106856  
<151> 1998-11-03

<150> 60/106902  
<151> 1998-11-03

<150> 60/106905  
<151> 1998-11-03

<150> 60/106919  
<151> 1998-11-03

<150> 60/106932  
<151> 1998-11-03

<150> 60/106934  
<151> 1998-11-03

<150> 60/107783  
<151> 1998-11-10

<150> 60/108775

<151> 1998-11-17

<150> 60/108779  
<151> 1998-11-17

<150> 60/108787  
<151> 1998-11-17

<150> 60/108788  
<151> 1998-11-17

<150> 60/108801  
<151> 1998-11-17

<150> 60/108802  
<151> 1998-11-17

<150> 60/108806  
<151> 1998-11-17

<150> 60/108807  
<151> 1998-11-17

<150> 60/108848  
<151> 1998-11-18

<150> 60/108849  
<151> 1998-11-18

<150> 60/108850  
<151> 1998-11-18

<150> 60/108851  
<151> 1998-11-18

<150> 60/108852  
<151> 1998-11-18

<150> 60/108858  
<151> 1998-11-18

<150> 60/108867  
<151> 1998-11-17

<150> 60/108904  
<151> 1998-11-18

<150> 60/108925  
<151> 1998-11-17

<150> 60/113296  
<151> 1998-12-22

<150> 60/114223  
<151> 1998-12-30

<150> 60/129674  
<151> 1999-04-16

<150> 60/141037  
<151> 1999-06-23

<150> 60/144758  
<151> 1999-07-20

<150> 60/145698  
<151> 1999-07-26

<150> 60/162506  
<151> 1999-10-29

<150> 09/218517  
<151> 1998-12-22

<150> 09/284291  
<151> 1999-04-12

<150> 09/403297  
<151> 1999-10-18

<150> 09/872035  
<151> 2001-06-01

<150> 09/882636  
<151> 2001-06-14

<150> PCT/US99/00106  
<151> 1999-01-05

<150> PCT/US99/20111  
<151> 1999-09-01

<150> PCT/US99/21194  
<151> 1999-09-15

<150> PCT/US99/28313  
<151> 1999-11-30

<150> PCT/US99/28551  
<151> 1999-12-02

<150> PCT/US99/30095  
<151> 1999-12-16

<150> PCT/US00/00219  
<151> 2000-01-05

<150> PCT/US00/00376  
<151> 2000-01-06

<150> PCT/US00/03565  
<151> 2000-02-11

<150> PCT/US00/04342  
<151> 2000-02-18

<150> PCT/US00/05004

<151> 2000-02-24

<150> PCT/US00/05841  
<151> 2000-03-02

<150> PCT/US00/06884  
<151> 2000-03-15

<150> PCT/US00/13705  
<151> 2000-05-17

<150> PCT/US00/14042  
<151> 2000-05-22

<150> PCT/US00/14941  
<151> 2000-05-30

<150> PCT/US00/15264  
<151> 2000-06-02

<150> PCT/US00/23328  
<151> 2000-08-24

<150> PCT/US00/23522  
<151> 2000-08-23

<150> PCT/US00/30873  
<151> 2000-11-10

<150> PCT/US00/30952  
<151> 2000-11-08

<150> PCT/US00/32678  
<151> 2000-12-01

<150> PCT/US01/06520  
<151> 2001-02-28

<150> PCT/US01/06666  
<151> 2001-03-01

<150> PCT/US01/17800  
<151> 2001-06-01

<150> PCT/US01/19692  
<151> 2001-06-20

<150> PCT/US01/21066  
<151> 2001-06-29

<150> PCT/US01/21735  
<151> 2001-07-09

<160> 477

<210> 1  
<211> 43  
<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Sequence - Artificial

<400> 1  
tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 2

<211> 41

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-41

<223> Sequence - Artificial

<400> 2  
caggaaacag ctatgaccac ctgcacacct gcaaatccat t 41

<210> 3

<211> 1110

<212> DNA

<213> Homo sapiens

<400> 3  
ccaatcgccc ggtgcggtgg tgcagggct cgggctagtc atggcgtccc 50  
cgtctcggag actgcagact aaaccagtca ttacttgttt caagagcgtt 100  
ctgctaattct acacttttat tttctggatc actggcgtta tccttcttgc 150  
agttggcatt tggggcaagg tgagcctgga gaattacttt tctctttaa 200  
atgagaaggc caccaatgtc cccttcgtgc tcattgtac tggtaccgtc 250  
attattcttt tgggcacatt tggttgttt gctacctgcc gagcttctgc 300  
atggatgcta aaactgtatg caatgtttct gactctcggtt ttttggtcg 350  
aactggtcgc tgccatcgta ggatttgttt tcagacatga gattaagaac 400  
agctttaaga ataattatga gaaggctttg aagcagtata actctacagg 450  
agattataga agccatgcag tagacaagat caaaaatacg ttgcattgtt 500  
gtgggtgcac cgattataga gattggacag atactaatta ttactcagaa 550  
aaaggatttc ctaagagttg ctgtaaactt gaagattgtt ctccacagag 600  
agatgcagac aaagtaaaaca atgaaggttg ttttataaaag gtgatgacca 650  
ttatagagtc agaaatggga gtcgttgcag gaatttcctt tggagttgtt 700  
tgcttccaac tgattggaat ctttctcgcc tactgccwct ctcgtgccat 750

aacaaataac cagtatgaga tagtgtaacc caatgttatct gtgggcstat 800  
tcctctctac cttaaggac atttagggc cccctgtga attagaaagt 850  
tgcttggctg gagaactgac aacactactt actgatagac caaaaaacta 900  
caccagtagg ttgattcaat caagatgtat gtagacctaa aactacacca 950  
ataggctgat tcaatcaaga tccgtgctcg cagttggctg attcaatcaa 1000  
gatgtatgtt tgctatgttc taagtccacc ttctatccca ttcatgttag 1050  
atcggtgaaa ccctgttatcc ctctgaaaca ctggaagagc tagtaaattg 1100  
taaatgaagt 1110

<210> 4  
<211> 245  
<212> PRT  
<213> Homo sapiens

<220>  
<221> sig\_peptide  
<222> 1-42  
<223> Signal Peptide

<220>  
<221> TRANSMEM  
<222> 19-42, 61-83, 92-114, 209-230  
<223> Transmembrane Domains

<220>  
<221> misc\_feature  
<222> 69-80, 211-222  
<223> Prokaryotic Membrane Lipoprotein Lipid Attachment Site.

<220>  
<221> misc\_feature  
<222> 75-81, 78-84, 210-216, 214-220, 226-232  
<223> N-Myristoylation Site.

<220>  
<221> misc\_feature  
<222> 134-138  
<223> N-Glycosylation Site.

<220>  
<221> misc\_feature  
<222> 160-168, 160-169  
<223> Tyrosine Kinase Phosphorylation Site.

<220>  
<221> unsure  
<222> 233  
<223> unknown amino acid

<400> 4  
Met Ala Ser Pro Ser Arg Arg Leu Gln Thr Lys Pro Val Ile Thr

1	5	10	15											
Cys	Phe	Lys	Ser	Val	Leu	Leu	Ile	Tyr	Thr	Phe	Ile	Phe	Trp	Ile
				20				25					30	
Thr	Gly	Val	Ile	Leu	Leu	Ala	Val	Gly	Ile	Trp	Gly	Lys	Val	Ser
				35				40					45	
Leu	Glu	Asn	Tyr	Phe	Ser	Leu	Leu	Asn	Glu	Lys	Ala	Thr	Asn	Val
				50				55					60	
Pro	Phe	Val	Leu	Ile	Ala	Thr	Gly	Thr	Val	Ile	Ile	Leu	Leu	Gly
				65				70					75	
Thr	Phe	Gly	Cys	Phe	Ala	Thr	Cys	Arg	Ala	Ser	Ala	Trp	Met	Leu
				80				85					90	
Lys	Leu	Tyr	Ala	Met	Phe	Leu	Thr	Leu	Val	Phe	Leu	Val	Glu	Leu
				95				100					105	
Val	Ala	Ala	Ile	Val	Gly	Phe	Val	Phe	Arg	His	Glu	Ile	Lys	Asn
				110				115					120	
Ser	Phe	Lys	Asn	Asn	Tyr	Glu	Lys	Ala	Leu	Lys	Gln	Tyr	Asn	Ser
				125				130					135	
Thr	Gly	Asp	Tyr	Arg	Ser	His	Ala	Val	Asp	Lys	Ile	Gln	Asn	Thr
				140				145					150	
Leu	His	Cys	Cys	Gly	Val	Thr	Asp	Tyr	Arg	Asp	Trp	Thr	Asp	Thr
				155				160					165	
Asn	Tyr	Tyr	Ser	Glu	Lys	Gly	Phe	Pro	Lys	Ser	Cys	Cys	Lys	Leu
				170				175					180	
Glu	Asp	Cys	Thr	Pro	Gln	Arg	Asp	Ala	Asp	Lys	Val	Asn	Asn	Glu
				185				190					195	
Gly	Cys	Phe	Ile	Lys	Val	Met	Thr	Ile	Ile	Glu	Ser	Glu	Met	Gly
				200				205					210	
Val	Val	Ala	Gly	Ile	Ser	Phe	Gly	Val	Ala	Cys	Phe	Gln	Leu	Ile
				215				220					225	
Gly	Ile	Phe	Leu	Ala	Tyr	Cys	Xaa	Ser	Arg	Ala	Ile	Thr	Asn	Asn
				230				235					240	
Gln	Tyr	Glu	Ile	Val										
				245										

<210> 5  
<211> 1218  
<212> DNA  
<213> Homo sapiens

<400> 5  
cccacgcgtc cggcgccgtg gcctcgcgtc catcttgcc gttctctcg 50

acctgtcaca aaggagtcgc gccgcccggc cgccccctc cctccggtgg 100  
gcccgaggagg tagagaaaagt cagtgcacca gcccgaccgc gctgctctga 150  
gccctggca cgcgaaacgg gagggagtct gagggttggg gacgtctgtg 200  
agggagggga acagccgctc gagcctgggg cggcgacc ggactggggc 250  
cgggtaggc tctggaaagg gcccggaga gaggtggcgt tggtcagaac 300  
ctgagaaaca gccgagaggt tttccaccga ggcccgcgct tgagggatct 350  
gaagaggttc ctagaagagg gtgtccctc ttcgggggt ctcaccaga 400  
agaggttctt ggggtcgcc cttctgagga ggctcgccgt aacagggccc 450  
agaactgcca ttggatgtcc agaatcccct gtagttgata atgttggaa 500  
taagctctgc aactttctt ggcattcagt tgtaaaaac aaataggatg 550  
caaattcctc aactccaggt tatgaaaaca gtacttgaa aactgaaaac 600  
tacctaaatg atcgtcttg gttggccgt gttcttagcg agcagaagcc 650  
ttggccaggg tctgttgtt actctcgaag agcacatagc ccacttccta 700  
gggactggag gtgccgtac taccatgggt aattcctgta tctgccgaga 750  
tgacagtggaa acagatgaca gtgttgacac ccaacagcaa cagggcggaga 800  
acagtgcagt acccactgct gacacaagga gccaaccacg ggaccctgtt 850  
cgcccaccaa ggagggccg aggacctcat gagccaagga gaaagaaaca 900  
aaatgtggat gggctagtgt tggacacact ggcagtaata cggactctg 950  
tagataagta agtatctgac tcacggtcac ctccagtggaa atgaaaagtg 1000  
ttctgcccgg aaccatgact ttaggactcc ttcaagttccct ttaggacata 1050  
ctcgccaagc cttgtgctca cagggcaaag gagaatattt taatgctcg 1100  
ctgatggcag agtaaatgat aagatttgat gttttgctt gctgtcatct 1150  
actttgtctg gaaatgtcta aatgtttctg tagcagaaaa cacgataaaag 1200  
ctatgatctt tattagag 1218

<210> 6  
<211> 117  
<212> PRT  
<213> Homo sapiens

<220>  
<221> sig\_peptide  
<222> 1-16  
<223> Signal Peptide

<220>  
 <221> misc\_feature  
 <222> 18-24, 32-38, 34-40, 35-41, 51-57  
 <223> N-Myristoylation Site.

<220>  
 <221> misc\_feature  
 <222> 22-26, 50-54, 113-117  
 <223> Casein Kinase II Phosphorylation Site.

<400> 6  
 Met Ile Val Phe Gly Trp Ala Val Phe Leu Ala Ser Arg Ser Leu  
 1 5 10 15

Gly Gln Gly Leu Leu Leu Thr Leu Glu Glu His Ile Ala His Phe  
 20 25 30

Leu Gly Thr Gly Gly Ala Ala Thr Thr Met Gly Asn Ser Cys Ile  
 35 40 45

Cys Arg Asp Asp Ser Gly Thr Asp Asp Ser Val Asp Thr Gln Gln  
 50 55 60

Gln Gln Ala Glu Asn Ser Ala Val Pro Thr Ala Asp Thr Arg Ser  
 65 70 75

Gln Pro Arg Asp Pro Val Arg Pro Pro Arg Arg Gly Arg Gly Pro  
 80 85 90

His Glu Pro Arg Arg Lys Lys Gln Asn Val Asp Gly Leu Val Leu  
 95 100 105

Asp Thr Leu Ala Val Ile Arg Thr Leu Val Asp Lys  
 110 115

<210> 7  
 <211> 756  
 <212> DNA  
 <213> Homo sapiens

<400> 7  
 ggcacgaggc gctgtccacc cggggcggt ggagttaggt accagattca 50  
 gcccatttgg ccccgacgcc tctgttctcg gaatccgggt gctgcggatt 100  
 gaggtccccgg ttcctaacctg actgcaagat ggaggaaggc gggAACCTAG 150  
 gaggcctgat taagatggtc catctactgg tcttgcagg tgcctgggc 200  
 atgcaaatgt gggtaacctt cgtctcaggc ttccctgcttt tccgaagcct 250  
 tccccgacat accttcggac tagtgcagag caaactcttc cccttctact 300  
 tccacatctc catggctgt gccttcatca acctctgcat ctggcttca 350  
 cagcatgctt gggctcagct cacattctgg gaggccagcc agctttacct 400  
 gctgttcctg agccttacgc tggccactgt caacgcccgc tggctgaaac 450

ccccgaccac agctgccatg tggccctgc aaaccgtgga gaaggagcga 500  
ggcctgggtg gggaggtacc aggccagccac cagggtcccg atccctaccc 550  
ccagctgcga gagaaggacc ccaagtacag tgctctccgc cagaatttct 600  
tccgctacca tgggctgtcc tctctttgca atctgggctg cgtcctgagc 650  
aatgggctct gtctcgctgg ctttgccctg gaaataagga gcctctagca 700  
tggccctgc atgctaataa atgcttcttc agaaatgaaa aaaaaaaaaa 750  
aaaaaa 756

<210> 8  
<211> 189  
<212> PRT  
<213> Homo sapiens

<220>  
<221> sig\_peptide  
<222> 1-24  
<223> Signal Peptide

<220>  
<221> misc\_feature  
<222> 4-10, 5-11, 47-53, 170-176, 176-182  
<223> N-Myristoylation Site.

<220>  
<221> misc\_feature  
<222> 44-85  
<223> G-protein Coupled Receptors Proteins.

<220>  
<221> misc\_feature  
<222> 54-65  
<223> Prokaryotic Mmembrane Lipoprotein Lipid Attachment Site.

<220>  
<221> misc\_feature  
<222> 82-86  
<223> Casein Kinase II Phosphorylation Site.

<220>  
<221> TRANSMEM  
<222> 86-103, 60-75  
<223> Transmembrane Domain

<220>  
<221> misc\_feature  
<222> 144-151  
<223> Tyrosine Kinase Phosphorylation Site.

<400> 8  
Met Glu Glu Gly Gly Asn Leu Gly Gly Leu Ile Lys Met Val His  
1 5 10 15

Leu	Leu	Val	Leu	Ser	Gly	Ala	Trp	Gly	Met	Gln	Met	Trp	Val	Thr
				20					25				30	
Phe	Val	Ser	Gly	Phe	Leu	Leu	Phe	Arg	Ser	Leu	Pro	Arg	His	Thr
				35					40				45	
Phe	Gly	Leu	Val	Gln	Ser	Lys	Leu	Phe	Pro	Phe	Tyr	Phe	His	Ile
				50					55				60	
Ser	Met	Gly	Cys	Ala	Phe	Ile	Asn	Leu	Cys	Ile	Leu	Ala	Ser	Gln
				65					70				75	
His	Ala	Trp	Ala	Gln	Leu	Thr	Phe	Trp	Glu	Ala	Ser	Gln	Leu	Tyr
				80					85				90	
Leu	Leu	Phe	Leu	Ser	Leu	Thr	Leu	Ala	Thr	Val	Asn	Ala	Arg	Trp
				95					100				105	
Leu	Glu	Pro	Arg	Thr	Thr	Ala	Ala	Met	Trp	Ala	Leu	Gln	Thr	Val
				110					115				120	
Glu	Lys	Glu	Arg	Gly	Leu	Gly	Gly	Glu	Val	Pro	Gly	Ser	His	Gln
				125					130				135	
Gly	Pro	Asp	Pro	Tyr	Arg	Gln	Leu	Arg	Glu	Lys	Asp	Pro	Lys	Tyr
				140					145				150	
Ser	Ala	Leu	Arg	Gln	Asn	Phe	Phe	Arg	Tyr	His	Gly	Leu	Ser	Ser
				155					160				165	
Leu	Cys	Asn	Leu	Gly	Cys	Val	Leu	Ser	Asn	Gly	Leu	Cys	Leu	Ala
				170					175				180	
Gly	Leu	Ala	Leu	Glu	Ile	Arg	Ser	Leu						
				185										

<210> 9  
<211> 1508  
<212> DNA  
<213> Homo sapiens

<400> 9  
aattcagatt ttaagccat tctgcagtgg aatttcatga actagcaaga 50  
ggacaccatc ttcttgtatt atacaagaaa ggagtgtacc tatcacacac 100  
agggggaaaa atgctttt gggtgctagg cctcctaatac ctctgtggtt 150  
ttctgtggac tcgtaaagga aaactaaaga ttgaagacat cactgataag 200  
tacatttta tcactggatg tgactcgggc tttggaaact tggcagccag 250  
aacttttgcataat aaaaaggat ttcatgtaat cgctgcctgt ctgactgaat 300  
caggatcaac agctttaaag gcagaaacct cagagagact tcgtactgt 350  
cttctggatg tgaccgaccc agagaatgtc aagaggactg cccagtggt 400

gaagaaccaa gttggggaga aaggctctg gggctgatc aataatgctg 450  
gtgttcccg cgtgctggct cccactgact ggctgacact agaggactac 500  
agagaaccta ttgaagtgaa cctgtttgga ctcatcagtg tgacactaaa 550  
tatgcttcct ttggtaaga aagctcaagg gagagttatt aatgtctcca 600  
gtgttggagg tcgccttgca atcggtggag gggctatac tccatccaaa 650  
tatgcagtgg aaggttcaa tgacagctt agacggaca tgaaagctt 700  
tggtgtgcac gtctcatgca ttgaaccagg attgttcaaa acaaacttgg 750  
cagatccagt aaaggtaatt gaaaaaaaaac tcgcatttg ggagcagctg 800  
tctccagaca tcaaacaaca atatggagaa gtttacattt aaaaaagtct 850  
agacaaactg aaaggcaata aatcctatgt gaacatggac ctctctccgg 900  
tggtagatgt catggaccac gctctaaca gtctcttccc taagactcat 950  
tatgccgctg gaaaagatgc caaaattttc tggatacctc tgtctcacat 1000  
gccagcagct ttgcaagact ttttattgtt gaaacagaaa gcagagctgg 1050  
ctaatcccaa ggcagtgtga ctcagctaac cacaaatgtc tcctccaggc 1100  
tatgaaattt gccgatttca agaacacatc tcctttcaa cccattcct 1150  
tatctgctcc aacctggact catttagatc gtgttattt ggattgcaaa 1200  
agggagtccc accatcgctg gtggtatccc agggtccctg ctcaagttt 1250  
cttgaaaag gagggctgga atggtacate acataggcaa gtcctgcct 1300  
gtattnaggc tttgcctgct tgggtgatg taaggaaat tgaaagactt 1350  
gcccattcaa aatgatctt accgtggcct gccccatgct tatggtcccc 1400  
agcatttaca gtaacttgg aatgttaagt atcatctt atctaaatat 1450  
taaaagataa gtcaacccaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500  
aaaaaaaa 1508

<210> 10  
<211> 319  
<212> PRT  
<213> Homo sapiens

<220>  
<221> sig\_peptide  
<222> 1-17  
<223> Signal Peptide

<220>  
<221> misc\_feature

<222> 36-47, 108-113, 166-171, 198-203, 207-212  
<223> N-myristoylation Sites.

<220>  
<221> misc\_feature

<222> 39-42

<223> Glycosaminoglycan Attachment Site.

<220>  
<221> TRANSMEM

<222> 136-152

<223> Transmembrane Domain

<220>

<221> misc\_feature

<222> 161-163, 187-190 and 253-256

<223> N-glycosylation Sites.

<400> 10

Met	Leu	Phe	Trp	Val	Leu	Gly	Leu	Leu	Ile	Leu	Cys	Gly	Phe	Leu
1				5					10					15

Trp	Thr	Arg	Lys	Gly	Lys	Leu	Lys	Ile	Glu	Asp	Ile	Thr	Asp	Lys
				20				25						30

Tyr	Ile	Phe	Ile	Thr	Gly	Cys	Asp	Ser	Gly	Phe	Gly	Asn	Leu	Ala
				35				40						45

Ala	Arg	Thr	Phe	Asp	Lys	Lys	Gly	Phe	His	Val	Ile	Ala	Ala	Cys
				50				55						60

Leu	Thr	Glu	Ser	Gly	Ser	Thr	Ala	Leu	Lys	Ala	Glu	Thr	Ser	Glu
				65				70						75

Arg	Leu	Arg	Thr	Val	Leu	Leu	Asp	Val	Thr	Asp	Pro	Glu	Asn	Val
				80				85						90

Lys	Arg	Thr	Ala	Gln	Trp	Val	Lys	Asn	Gln	Val	Gly	Glu	Lys	Gly
				95				100						105

Leu	Trp	Gly	Leu	Ile	Asn	Asn	Ala	Gly	Val	Pro	Gly	Val	Leu	Ala
				110				115						120

Pro	Thr	Asp	Trp	Leu	Thr	Leu	Glu	Asp	Tyr	Arg	Glu	Pro	Ile	Glu
				125				130						135

Val	Asn	Leu	Phe	Gly	Leu	Ile	Ser	Val	Thr	Leu	Asn	Met	Leu	Pro
				140				145						150

Leu	Val	Lys	Lys	Ala	Gln	Gly	Arg	Val	Ile	Asn	Val	Ser	Ser	Val
				155				160						165

Gly	Gly	Arg	Leu	Ala	Ile	Val	Gly	Gly	Tyr	Thr	Pro	Ser	Lys	
				170				175						180

Tyr	Ala	Val	Glu	Gly	Phe	Asn	Asp	Ser	Leu	Arg	Arg	Asp	Met	Lys
				185				190						195

Ala Phe Gly Val His Val Ser Cys Ile Glu Pro Gly Leu Phe Lys  
 200 205 210  
 Thr Asn Leu Ala Asp Pro Val Lys Val Ile Glu Lys Lys Leu Ala  
 215 220 225  
 Ile Trp Glu Gln Leu Ser Pro Asp Ile Lys Gln Gln Tyr Gly Glu  
 230 235 240  
 Gly Tyr Ile Glu Lys Ser Leu Asp Lys Leu Lys Gly Asn Lys Ser  
 245 250 255  
 Tyr Val Asn Met Asp Leu Ser Pro Val Val Glu Cys Met Asp His  
 260 265 270  
 Ala Leu Thr Ser Leu Phe Pro Lys Thr His Tyr Ala Ala Gly Lys  
 275 280 285  
 Asp Ala Lys Ile Phe Trp Ile Pro Leu Ser His Met Pro Ala Ala  
 290 295 300  
 Leu Gln Asp Phe Leu Leu Leu Lys Gln Lys Ala Glu Leu Ala Asn  
 305 310 315  
 Pro Lys Ala Val

<210> 11  
 <211> 2720  
 <212> DNA  
 <213> Homo sapines

<400> 11  
 gcgggctgtt gacggcgctg cgatggctgc ctgcgagggc aggagaagcg 50  
 gagctctcg ttcctcttag tcggacttcc tgacgcccgc agtgggcggg 100  
 gccccttggg ccgtcgccac cactgttagtc atgtacccac cggccggcc 150  
 gccgcctcat cgggacttca tctcggtgac gctgagctt ggcgagagct 200  
 atgacaacag caagagttgg cggcggcgct cgtgctggag gaaatggaag 250  
 caactgtcga gattgcagcg gaatatgatt ctcttcctcc ttgcctttct 300  
 gctttctgt ggactcctct tctacatcaa cttggctgac cattggaaag 350  
 ctctggcttt caggcttagag gaagagcaga agatgaggcc agaaattgct 400  
 gggtaaaac cagcaaattcc acccgcttta ccagctcctc agaaggcgga 450  
 caccgaccct gagaacttac ctgagatttc gtcacagaag acacaaagac 500  
 acatccagcg gggaccaccc cacctgcaga ttagacccccc aagccaagac 550  
 ctgaaggatg ggaccacccgg aaggccaca aaaaggcaag aagcccttgt 600  
 ggatccccgc ccggaaggag atcccgagag gacagtcatc agctggaggg 650

gagcggtgat cgagcctgag cagggcacccg agctcccttc aagaagagca 700  
gaagtgccca ccaaggctcc cctgccacccg gccaggacac agggcacacc 750  
agtgcacatcg aactatcgcc agaagggcgt gattgacgac ttcctgcatg 800  
catggaaagg ataccgcaag tttgcatggg gccatgacga gctgaaggct 850  
gtgtccaggt cttcagtga gtgggttggc ctccggctca cactgatcga 900  
cgcgctggac accatgtgga tcttgggtct gagaaaagaa tttgaggaag 950  
ccaggaagtg ggtgtcgaag aagttacact ttgaaaagga cgtggacgac 1000  
aacctgtttg agagcacgat ccgcacatcctg gggggctcc tgagtgccta 1050  
ccacctgtct ggggacagcc tcttccttag gaaagctgag gatttggaa 1100  
atcggttaat gcctgccttc agaacaccat ccaagattcc ttactcgat 1150  
gtgaacatcg gtactggagt tgcccacccg ccacggtgga cctccgacag 1200  
cactgtggcc gaggtgacca gcattcagct ggagttccgg gagctctccc 1250  
gtctcacagg ggataagaag tttcaggagg cagtggagaa ggtgacacag 1300  
cacatccacg gcctgtctgg gaagaaggat gggctggtgc ccatgttcat 1350  
caatacccac agtggctct tcacccaccc gggcgtattc acgctggcg 1400  
ccagggccga cagctactat gagtacctgc tgaagcagtg gatccaggc 1450  
gggaagcagg agacacagct gctggaagac tacgtggaag ccatcgaggg 1500  
tgtcagaacg cacctgctgc ggcactccga gcccagtaag ctcacctttg 1550  
tgggggagct tgccccacggc cgcttcagtg ccaagatgga ccacctggtg 1600  
tgcttcctgc cagggacgct ggctctgggc gtctaccacg gcctgccccgc 1650  
cagccacatg gagctggccc aggagctcat ggagacttgt taccagatga 1700  
accggcagat ggagacgggg ctgagtcggc agatcgtgca cttcaacctt 1750  
taccccccagc cggggccgtcg ggacgtggag gtcaagccag cagacaggca 1800  
caacctgctg cggccagaga ccgtggagag cctgttctac ctgtaccgcg 1850  
tcacagggga ccgcaaatac caggactggg gctggagat tctgcagagc 1900  
ttcagccgat tcacacgggt cccctcggtt ggctattctt ccatcaacaa 1950  
tgtccaggat cctcagaagc ccgagcctag ggacaagatg gagagcttct 2000  
tcctggggga gacgctcaag tatctgttct tgctttctc cgatgaccca 2050  
aacctgctca gcctggacgc ctacgtgttc aacaccgaag cccaccctct 2100

gcctatctgg acccctgcct agggtggatg gctgctggtg tggggacttc 2150  
 gggtgggcag aggcaccttg ctgggtctgt ggcattttcc aagggccac 2200  
 gtagcaccgg caaccgccaa gtggcccagg ctctgaactg gctctggct 2250  
 ctcctcgta tctgctttaa tcaggacacc gtgaggacaä gtgaggccgt 2300  
 cagtcttgggt gtgatgcggg gtgggctggg ccgctggagc ctccgcctgc 2350  
 ttccctccaga agacacgaat catgactcac gattgctgaa gcctgagcag 2400  
 gtctctgtgg gccgaccaga gggggcttc gaggtggtcc ctggtaactgg 2450  
 ggtgaccgag tggacagccc agggtgcagc tctgcccggg ctcgtgaagc 2500  
 ctcagatgtc cccaatccaa gggctggag gggctgccgt gactccagag 2550  
 gcctgaggct ccagggctgg ctctgggtt tacaagctgg actcagggat 2600  
 ctcctggcc gccccgcagg gggcttggag ggctggacgg caagtccgtc 2650  
 tagctcacgg gcccctccag tggaaatgggt ctttcgggt gagataaaaag 2700  
 ttgatttgct ctaaccgcaa 2720

<210> 12  
 <211> 699  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> TRANSMEM  
 <222> 21-40 and 84-105  
 <223> Transmembrane Domain (type II)

<400> 12  
 Met Ala Ala Cys Glu Gly Arg Arg Ser Gly Ala Leu Gly Ser Ser  
   1                       5                                   10                           15  
 Gln Ser Asp Phe Leu Thr Pro Pro Val Gly Gly Ala Pro Trp Ala  
   20   25                                   30  
 Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro Pro  
   35   40                                   45  
 His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr  
   50   55                                   60  
 Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp  
   65   70                                   75  
 Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu  
   80   85                                   90  
 Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala  
   95   100                                   105

Asp His Trp Lys Ala Leu Ala Phe Arg Leu Glu Glu Glu Gln Lys  
 110 115 120  
 Met Arg Pro Glu Ile Ala Gly Leu Lys Pro Ala Asn Pro Pro Val  
 125 130 135  
 Leu Pro Ala Pro Gln Lys Ala Asp Thr Asp Pro Glu Asn Leu Pro  
 140 145 150  
 Glu Ile Ser Ser Gln Lys Thr Gln Arg His Ile Gln Arg Gly Pro  
 155 160 165  
 Pro His Leu Gln Ile Arg Pro Pro Ser Gln Asp Leu Lys Asp Gly  
 170 175 180  
 Thr Gln Glu Glu Ala Thr Lys Arg Gln Glu Ala Pro Val Asp Pro  
 185 190 195  
 Arg Pro Glu Gly Asp Pro Gln Arg Thr Val Ile Ser Trp Arg Gly  
 200 205 210  
 Ala Val Ile Glu Pro Glu Gln Gly Thr Glu Leu Pro Ser Arg Arg  
 215 220 225  
 Ala Glu Val Pro Thr Lys Pro Pro Leu Pro Pro Ala Arg Thr Gln  
 230 235 240  
 Gly Thr Pro Val His Leu Asn Tyr Arg Gln Lys Gly Val Ile Asp  
 245 250 255  
 Val Phe Leu His Ala Trp Lys Gly Tyr Arg Lys Phe Ala Trp Gly  
 260 265 270  
 His Asp Glu Leu Lys Pro Val Ser Arg Ser Phe Ser Glu Trp Phe  
 275 280 285  
 Gly Leu Gly Leu Thr Leu Ile Asp Ala Leu Asp Thr Met Trp Ile  
 290 295 300  
 Leu Gly Leu Arg Lys Glu Phe Glu Glu Ala Arg Lys Trp Val Ser  
 305 310 315  
 Lys Lys Leu His Phe Glu Lys Asp Val Asp Val Asn Leu Phe Glu  
 320 325 330  
 Ser Thr Ile Arg Ile Leu Gly Gly Leu Leu Ser Ala Tyr His Leu  
 335 340 345  
 Ser Gly Asp Ser Leu Phe Leu Arg Lys Ala Glu Asp Phe Gly Asn  
 350 355 360  
 Arg Leu Met Pro Ala Phe Arg Thr Pro Ser Lys Ile Pro Tyr Ser  
 365 370 375  
 Asp Val Asn Ile Gly Thr Gly Val Ala His Pro Pro Arg Trp Thr  
 380 385 390  
 Ser Asp Ser Thr Val Ala Glu Val Thr Ser Ile Gln Leu Glu Phe

395	400	405
Arg Glu Leu Ser Arg Leu Thr Gly Asp Lys Lys Phe Gln Glu Ala		
410	415	420
Val Glu Lys Val Thr Gln His Ile His Gly Leu Ser Gly Lys Lys		
425	430	435
Asp Gly Leu Val Pro Met Phe Ile Asn Thr His Ser Gly Leu Phe		
440	445	450
Thr His Leu Gly Val Phe Thr Leu Gly Ala Arg Ala Asp Ser Tyr		
455	460	465
Tyr Glu Tyr Leu Leu Lys Gln Trp Ile Gln Gly Gly Lys Gln Glu		
470	475	480
Thr Gln Leu Leu Glu Asp Tyr Val Glu Ala Ile Glu Gly Val Arg		
485	490	495
Thr His Leu Leu Arg His Ser Glu Pro Ser Lys Leu Thr Phe Val		
500	505	510
Gly Glu Leu Ala His Gly Arg Phe Ser Ala Lys Met Asp His Leu		
515	520	525
Val Cys Phe Leu Pro Gly Thr Leu Ala Leu Gly Val Tyr His Gly		
530	535	540
Leu Pro Ala Ser His Met Glu Leu Ala Gln Glu Leu Met Glu Thr		
545	550	555
Cys Tyr Gln Met Asn Arg Gln Met Glu Thr Gly Leu Ser Pro Glu		
560	565	570
Ile Val His Phe Asn Leu Tyr Pro Gln Pro Gly Arg Arg Asp Val		
575	580	585
Glu Val Lys Pro Ala Asp Arg His Asn Leu Leu Arg Pro Glu Thr		
590	595	600
Val Glu Ser Leu Phe Tyr Leu Tyr Arg Val Thr Gly Asp Arg Lys		
605	610	615
Tyr Gln Asp Trp Gly Trp Glu Ile Leu Gln Ser Phe Ser Arg Phe		
620	625	630
Thr Arg Val Pro Ser Gly Gly Tyr Ser Ser Ile Asn Asn Val Gln		
635	640	645
Asp Pro Gln Lys Pro Glu Pro Arg Asp Lys Met Glu Ser Phe Phe		
650	655	660
Leu Gly Glu Thr Leu Lys Tyr Leu Phe Leu Leu Phe Ser Asp Asp		
665	670	675
Pro Asn Leu Leu Ser Leu Asp Ala Tyr Val Phe Asn Thr Glu Ala		
680	685	690

His Pro Leu Pro Ile Trp Thr Pro Ala  
695

<210> 13  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 13  
cgccagaagg gcgtgattga cgtc 24

<210> 14  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 14  
ccatccttct tcccagacag gccg 24

<210> 15  
<211> 44  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-44  
<223> Synthetic construct.

<400> 15  
gaagcctgtg tccaggtcct tcagtgagtg gtttggcctc ggtc 44

<210> 16  
<211> 1524  
<212> DNA  
<213> Homo sapiens

<400> 16  
ggcgccgcgt aggccccggga ggccgggccc gcccggctgc gagcgcctgc 50  
cccatgcgcc gccgcctctc cgcacgatgt tcccctcgcg gagaaagcg 100  
gcgcagctgc cctgggagga cggcaggtcc gggttgctct ccggcggcct 150  
ccctcggaag tggccgtct tccacctgtt cgtggcctgc ctctcgctgg 200  
gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250

cgggcagtca ggggacaagg gcaggagacc tcggccctc cccgtgcctg 300  
cccccccagag ccgccccctg agcaactggga agaagacgca tcctggggcc 350  
cccaccgcct ggcagtgctg gtgcccttcc gcgaacgctt cgaggagctc 400  
ctggtcttcg tgccccacat gcgcgccttc ctgagcagga agaagatccg 450  
gcaccacatc tacgtgctca accaggtgga ccacttcagg ttcaaccggg 500  
cagcgctcat caacgtggc ttcctggaga gcagcaacag cacggactac 550  
attgccatgc acgacgttga cctgctccct ctcaacgagg agctggacta 600  
tggcttcctt gaggctggc cttccacgt ggcctcccg gagctccacc 650  
ctctctacca ctacaagacc tatgtcggcg gcacccctgct gctctccaag 700  
cagcaactacc ggctgtgcaa tgggatgtcc aaccgcttct gggctgggg 750  
ccgcgaggac gacgagttct accggcgcat taagggagct gggctccagc 800  
tttccgccc ctcggaaatc acaactgggt acaagacatt tcgcccacgt 850  
catgacccag cctggcgaa gagggaccag aagcgcatcg cagctaaaaa 900  
acaggagcag ttcaaggtgg acagggaggg aggctgaac actgtgaagt 950  
accatgtggc ttcccgact gccctgtctg tgggggggc cccctgcact 1000  
gtcctcaaca tcatgttga ctgtgacaag accgcccacac cctggtgac 1050  
attcagctga gctggatgga cagtgagggaa gcctgtacct acaggccata 1100  
ttgctcaggc tcaggacaag gcctcaggtc gtggggccag ctctgacagg 1150  
atgtggagtg gccaggacca agacagcaag ctacgcaatt gcagccaccc 1200  
ggccgccaag gcaggcttgg gctggggccag gacacgtggg gtgcctggg 1250  
cgctgcttgc catgcacagt gatcagagag aggctgggt gtgtcctgtc 1300  
cgggacccccc cctgccttcc tgctcacccct actctgaccc cttcacgt 1350  
cccaggcctg tggtagtgg ggagggctga acaggacaac ctctcatcac 1400  
cctactctga ctccttcac gtgcggcaggc ctgtgggtag tggggaggc 1450  
tgaacaggac aacctctcat caccccaaaa aaaaaaaaaa aaaaaaaaaa 1500  
aaaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17  
<211> 327  
<212> PRT  
<213> Homo sapiens  
  
<220>

<221> sig\_peptide  
 <222> 1-42  
 <223> Signal peptide.  
  
 <220>  
 <221> misc\_feature  
 <222> 19-25, 65-71, 247-253, 285-291, 303-310  
 <223> N-myristoylation site.  
  
 <220>  
 <221> misc\_feature  
 <222> 27-31  
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.  
  
 <220>  
 <221> TRANSMEM  
 <222> 29-49  
 <223> Transmembrane domain (type II).  
  
 <220>  
 <221> misc\_feature  
 <222> 154-158  
 <223> N-glycosylation site.  
  
 <220>  
 <221> misc\_feature  
 <222> 226-233  
 <223> Tyrosine kinase phosphorylation site.  
  
 <400> 17  
 Met Phe Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp  
     1              5                 10                         15  
  
 Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser  
     20                 25                                 30  
  
 Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser  
     35                 40                                45  
  
 Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala  
     50                 55                                60  
  
 Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys  
     65                 70                                75  
  
 Pro Pro Glu Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp  
     80                 85                                90  
  
 Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe  
     95                 100                             105  
  
 Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser  
    110                 115                         120  
  
 Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp  
    125                 130                         135  
  
 His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu

140	145	150
Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala Met His Asp Val Asp		
155	160	165
Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly Phe Pro Glu Ala		
170	175	180
Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro Leu Tyr His		
185	190	195
Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys Gln His		
200	205	210
Tyr Arg Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp Gly		
215	220	225
Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu		
230	235	240
Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe		
245	250	255
Arg His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg		
260	265	270
Ile Ala Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly		
275	280	285
Gly Leu Asn Thr Val Lys Tyr His Val Ala Ser Arg Thr Ala Leu		
290	295	300
Ser Val Gly Gly Ala Pro Cys Thr Val Leu Asn Ile Met Leu Asp		
305	310	315
Cys Asp Lys Thr Ala Thr Pro Trp Cys Thr Phe Ser		
320	325	

<210> 18  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 18  
gcgaacgctt cgaggagtcc tgg 23

<210> 19  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence

<222> 1-24  
<223> Synthetic construct

<400> 19  
gcagtgcggg aagccacatg gtac 24

<210> 20  
<211> 46  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-46  
<223> Synthetic construct.

<400> 20  
cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21  
<211> 494  
<212> DNA  
<213> Homo sapiens

<400> 21  
caatgtttgc ctatccacct cccccaagcc ccttaccta tgctgctgct 50  
aacgctgctg ctgctgctgc tgctgcttaa aggctcatgc ttggagtggg 100  
gactggtcgg tgcccagaaa gtctcttctg ccactgacgc ccccatcagg 150  
gattgggcct tctttcccccc ttcccttctg tgtctcctgc ctcatcgcc 200  
tgccatgacc tgcagccaag cccagccccc tggggaaaggg gagaaagtgg 250  
gggatggcta agaaagctgg gagataggga acagaagagg gtagtgggtg 300  
ggctaggggg gctgccttat ttaaagtggt tgtttatgat tcttatacta 350  
atttatacaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400  
cctgtgttca atgtttgtaa agattgttct gtgtaaatat gtctttataa 450  
taaacagttt aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22  
<211> 73  
<212> PRT  
<213> Homo sapiens

<220>  
<221> sig peptide  
<222> 1-15  
<223> Signal peptide.

<220>  
<221> misc\_feature  
<222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22  
 Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Leu Lys Gly  
 1 5 10 15

Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser  
 20 25 30

Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser  
 35 40 45

Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln  
 50 55 60

Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly  
 65 70

<210> 23  
<211> 2883  
<212> DNA  
<213> Homo sapiens

<400> 23  
 gggacccatg cggccgtgac ccccggctcc ctagaggccc agcgcagccg 50  
 cagcggacaa aggagcatgt ccgcgccggg gaaggcccgt cctccggccg 100  
 ccataaggct ccggtcgccc ctgggccccg gccgcgtcc tgcccgcccc 150  
 ggctccgggg cgccccgcta gcccaagtgcg ccgcgcgtcg ccccgccaggc 200  
 cccggccccgc agcatggagc cacccggacg ccggcggggc cgcgcgcagc 250  
 cggcgctgtt gctgcgcgtc tcgctgttag cgctgctcgc gctgctggga 300  
 ggcggcggcg gcggcggcgcc cgccgcgtg cccggccgt gcaagcacga 350  
 tgggcggccc cgaggggctg gcagggcggc gggcgccgccc gagggcaagg 400  
 tggtgtgcag cagcctggaa ctcgcgcagg tcctgcccc agatactctg 450  
 cccaaccgca cggtcaccct gattctgagt aacaataaga tatccgagct 500  
 gaagaatggc tcattttctg ggttaagtct cttgaaaga ttggacactcc 550  
 gaaacaatct tatttagtagt atagatccag gtgccttctg gggactgtca 600  
 tctctaaaaa gattggatct gacaaacaat cgaataggat gtctgaatgc 650  
 agacatattt cgaggactca ccaatctggt tcggctaaac ctttcgggg 700  
 atttggatcttca ttcattatct caaggaacct ttgattatct tgcgtcatta 750  
 cggtctttgg aattccagac tgagtatct ttgtgtgact gtaacataact 800  
 gtggatgcat cgctggtaa aggagaagaa catcacggta cgggataccca 850

ggtgtgttta tcctaagtca ctgcaggccc aaccagtac accaggtaag 900  
caggagctgt tgacatgcga ccctccgctt gaattgccgt ctttctacat 950  
gactccatct catcgccaag ttgtgtttga aggagacagc cttcctttcc 1000  
agtgcattggc ttcataatatt gatcaggaca tgcaagtgtt gtggtatcat 1050  
gatgggagaa tagttgaaac cgatgaatcg caaggatatt ttgttgaaaa 1100  
gaacatgatt cacaactgct ctttgattgc aagtgcctta accatttcta 1150  
atattcaggc tggatctact ggaaattggg gctgtcatgt ccagacaaaa 1200  
cgtggaaata atacgaggac tgtggatatt gtggatttag agagttctgc 1250  
acagtaactgt cctccagaga ggggtggtaaa caacaaaggt gacttcagat 1300  
ggcccagaac attggcaggc attactgcat atctgcagt tacgcggaac 1350  
accatggca gtggatata tcccgaaac ccacaggatg agagaaaagc 1400  
ttggcgcaga tgtgatagag gtggcttttgcgcagatgat gattattctc 1450  
gctgtcagta tgcaaataatgat gtcactagag ttctttatat gtttaatcag 1500  
atgcccctca atcttaccaa tgccgtggca acagctcgac agttactggc 1550  
ttacactgtg gaagcagcca actttctga caaaatggat gttatatttgc 1600  
tggcagaaat gattaaaaaaa ttggaagat ttaccaagga gaaaaaatca 1650  
aaagagctag gtgacgtgat gttgacatt gcaagtaaca tcatgttggc 1700  
tgcgtacgt gtcctgtggc tggcgcagag ggaagctaaa gcctgcagta 1750  
ggatttgca gtgtcttcag cgcattgcta cctaccggct agccggtgga 1800  
gctcacgtt attcaacata ttccccaaat attgctctgg aagctttagt 1850  
catcaagtct actggcttca cggggatgac ctgtaccgtg ttccagaaag 1900  
tggcagcctc tgatcgtaca ggactttcg attatggag gcgggatcca 1950  
gagggaaacc tggataagca gctgagctt aagtgcattg tttcaaatac 2000  
attttcgagt ctggcactaa aggtatgtt cattctgca tcatttaaga 2050  
ctatttacag ttaaattaga atgctccaaa tggtctgctt cgcaaaataa 2100  
ccttattaaa agatttttt ttgcaggaag ataggatata ttgctttgc 2150  
tactgtttta aagaaaaacta accaggaaga actgcattac gactttcaag 2200  
ggcccttaggc attttgccct ttgattccct ttcttcacat aaaaatatca 2250  
gaaattacat ttataactg cagtggtata aatgcaaata tactattgtt 2300

acatgtgaaa aaattttatt tgacttaaaa gtttatttat ttgtttttt 2350  
 gctcctgatt ttaagacaat aagatgttt catggccccc taaaagtatc 2400  
 atgagcctt ggcactgcgc ctgccaaggcc tagtgagaa gtcaaccctg 2450  
 agaccaggtg tttaatcaag caagctgtat atcaaaattt ttggcagaaa 2500  
 acacaaatat gtcataatc ttttttaaa aaaagtattt cattgaagca 2550  
 agcaaaatga aagcattttt actgattttt aaaattggtg cttagatat 2600  
 atttgactac actgtattga agcaaataga ggaggcacaa ctccagcacc 2650  
 ctaatggaac cacatfffft tcacttagct ttctgtggc atgtgtatt 2700  
 gtattctctg cggttttaa tctcacagta ctttatttct gtcttgtccc 2750  
 tcaataatat cacaaacaat attccagtca ttttaatggc tgcataataa 2800  
 ctgatccaac aggtgttagg tgttctggtt tagtgtgagc actcaataaa 2850  
 tattgaatga atgaacgaaa aaaaaaaaaaaa aaa 2883

<210> 24  
 <211> 616  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> sig\_peptide  
 <222> 1-33  
 <223> Signal peptide.

<220>  
 <221> TRANSMEM  
 <222> 13-40  
 <223> Transmembrane domain (type II).

<400> 24  
 Met Glu Pro Pro Gly Arg Arg Arg Gly Ala Gln Pro Pro Leu  
     1               5                         10                  15  
 Leu Leu Pro Leu Ser Leu Leu Ala Leu Leu Ala Leu Gly Gly  
     20                 25   30  
 Gly Gly Gly Gly Ala Ala Ala Leu Pro Ala Gly Cys Lys His  
     35                 40  45  
 Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu  
     50                 55                                  60  
 Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro  
     65                 70                                 75  
 Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn  
     80                 85                                 90

Asn Lys Ile Ser Glu Leu Lys Asn Gly Ser Phe Ser Gly Leu Ser  
                   95                  100                  105  
 Leu Leu Glu Arg Leu Asp Leu Arg Asn Asn Leu Ile Ser Ser Ile  
                   110                  115                  120  
 Asp Pro Gly Ala Phe Trp Gly Leu Ser Ser Leu Lys Arg Leu Asp  
                   125                  130                  135  
 Leu Thr Asn Asn Arg Ile Gly Cys Leu Asn Ala Asp Ile Phe Arg  
                   140                  145                  150  
 Gly Leu Thr Asn Leu Val Arg Leu Asn Leu Ser Gly Asn Leu Phe  
                   155                  160                  165  
 Ser Ser Leu Ser Gln Gly Thr Phe Asp Tyr Leu Ala Ser Leu Arg  
                   170                  175                  180  
 Ser Leu Glu Phe Gln Thr Glu Tyr Leu Leu Cys Asp Cys Asn Ile  
                   185                  190                  195  
 Leu Trp Met His Arg Trp Val Lys Glu Lys Asn Ile Thr Val Arg  
                   200                  205                  210  
 Asp Thr Arg Cys Val Tyr Pro Lys Ser Leu Gln Ala Gln Pro Val  
                   215                  220                  225  
 Thr Gly Val Lys Gln Glu Leu Leu Thr Cys Asp Pro Pro Leu Glu  
                   230                  235                  240  
 Leu Pro Ser Phe Tyr Met Thr Pro Ser His Arg Gln Val Val Phe  
                   245                  250                  255  
 Glu Gly Asp Ser Leu Pro Phe Gln Cys Met Ala Ser Tyr Ile Asp  
                   260                  265                  270  
 Gln Asp Met Gln Val Leu Trp Tyr Gln Asp Gly Arg Ile Val Glu  
                   275                  280                  285  
 Thr Asp Glu Ser Gln Gly Ile Phe Val Glu Lys Asn Met Ile His  
                   290                  295                  300  
 Asn Cys Ser Leu Ile Ala Ser Ala Leu Thr Ile Ser Asn Ile Gln  
                   305                  310                  315  
 Ala Gly Ser Thr Gly Asn Trp Gly Cys His Val Gln Thr Lys Arg  
                   320                  325                  330  
 Gly Asn Asn Thr Arg Thr Val Asp Ile Val Val Leu Glu Ser Ser  
                   335                  340                  345  
 Ala Gln Tyr Cys Pro Pro Glu Arg Val Val Asn Asn Lys Gly Asp  
                   350                  355                  360  
 Phe Arg Trp Pro Arg Thr Leu Ala Gly Ile Thr Ala Tyr Leu Gln  
                   365                  370                  375  
 Cys Thr Arg Asn Thr His Gly Ser Gly Ile Tyr Pro Gly Asn Pro

380	385	390
Gln Asp Glu Arg Lys Ala Trp Arg Arg Cys	Asp Arg Gly Gly Phe	
395	400	405
Trp Ala Asp Asp Asp Tyr Ser Arg Cys Gln	Tyr Ala Asn Asp Val	
410	415	420
Thr Arg Val Leu Tyr Met Phe Asn Gln Met	Pro Leu Asn Leu Thr	
425	430	435
Asn Ala Val Ala Thr Ala Arg Gln Leu	Leu Ala Tyr Thr Val Glu	
440	445	450
Ala Ala Asn Phe Ser Asp Lys Met Asp Val	Ile Phe Val Ala Glu	
455	460	465
Met Ile Glu Lys Phe Gly Arg Phe Thr Lys	Glu Glu Lys Ser Lys	
470	475	480
Glu Leu Gly Asp Val Met Val Asp Ile Ala	Ser Asn Ile Met Leu	
485	490	495
Ala Asp Glu Arg Val Leu Trp Leu Ala Gln	Arg Glu Ala Lys Ala	
500	505	510
Cys Ser Arg Ile Val Gln Cys Leu Gln Arg	Ile Ala Thr Tyr Arg	
515	520	525
Leu Ala Gly Gly Ala His Val Tyr Ser Thr	Tyr Ser Pro Asn Ile	
530	535	540
Ala Leu Glu Ala Tyr Val Ile Lys Ser Thr	Gly Phe Thr Gly Met	
545	550	555
Thr Cys Thr Val Phe Gln Lys Val Ala	Ala Ser Asp Arg Thr Gly	
560	565	570
Leu Ser Asp Tyr Gly Arg Arg Asp Pro Glu	Gly Asn Leu Asp Lys	
575	580	585
Gln Leu Ser Phe Lys Cys Asn Val Ser Asn	Thr Phe Ser Ser Leu	
590	595	600
Ala Leu Lys Val Cys Tyr Ile Leu Gln Ser	Phe Lys Thr Ile Tyr	
605	610	615
Ser		

<210> 25  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24

<223> Synthetic construct

<400> 25

gaggactcac caatctgggtt cggc 24

<210> 26

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 26

aactggaaag gaaggctgtc tccc 24

<210> 27

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 27

gttaaaggaga agaacatcac ggtacggat accaggtgtg tttatcctaa 50

<210> 28

<211> 683

<212> DNA

<213> Homo sapiens

<400> 28

gcgtggggat gtctaggagc tcgaagggtgg tgctgggcct ctgggtgctg 50

ctgacggcgg ccacagtggc cggcgatcat gtgaagcagc agtgggacca 100

gcagaggctt cgtacggag ttatcagaga cattgagagg caaattcgg 150

aaaaagaaaa cattcgtctt ttgggagaac agattattt gactgagcaa 200

cttgaagcag aaagagagaa gatgttattt gcaaaaaggat ctcaaaaatc 250

atgacttgaa tgtgaaatat ctgttggaca gacaacacga gtttgtgtgt 300

gtgtgtttagt ggagagtagc ttagtagtat cttcatctt tttttggtc 350

actgtccttt taaacttgat caaataaagg acagtgggtc atataagtta 400

ctgctttcag ggtcccttat atctgaataa aggagtgtgg gcagacactt 450

tttggaaagag tctgtctggg tgatcctggt agaagccccca ttagggtcac 500

tgtccagtgc ttagggttgt tactgagaag cactgccgag cttgtgagaa 550

ggaaggggatg gatagtagca tccacacctgag tagtctgatc agtcggcatg 600  
atgacgaagc cacgagaaca tcgacacctgaa aaggactgga ggaagggtgaa 650  
gtggagggag agacgctcct gatcgctcgaa tcc 683

<210> 29  
<211> 81  
<212> PRT  
<213> Homo sapiens

<220>  
<221> sig\_peptide  
<222> 1-21  
<223> Signal peptide.

<400> 29  
Met Ser Arg Ser Ser Lys Val Val Leu Gly Leu Ser Val Leu Leu  
1 5 10 15

Thr Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp  
20 25 30

Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln  
35 40 45

Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile  
50 55 60

Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala  
65 70 75

Lys Gly Ser Gln Lys Ser  
80

<210> 30  
<211> 2128  
<212> DNA  
<213> Homo sapiens

<400> 30  
ctgtcgtctt tgcttcagcc gcagtcgcca ctggctgcct gaggtgctct 50  
tacagcctgt tccaaagtgtg gcttaatccg tctccaccac cagatcttc 100  
tccgtggatt cctctgctaa gaccgctgcc atgccagtga cggttaacccg 150  
caccaccatc acaaccacca cgacgtcatac ttccggcctg gggccccca 200  
tgatcgtggg gtcccccctcg gcccctgacac agcccccctggg tctcccttcgc 250  
ctgctgcagc tggtgtctac ctgcgtggcc ttctcgctgg tggctagcgt 300  
gggcgcctgg acggggtcca tgggcaactg gtccatgttc acctgggtgct 350  
tctgcttctc cgtgaccctg atcatcctca tcgtggagct gtgcgggctc 400  
caggccccgct tccccctgtc ttggcgcaac ttccccatca ctttcgcctg 450

ctatgcggcc ctcttctgcc ttcgcgcctc catcatctac cccaccaccc 500  
atgtccagtt cctgtcccac ggccgttgcg gggaccacgc catcgccgcc 550  
accttcttct cctgcacatgc gtgtgtggct tacgccaccg aagtggcctg 600  
gaccggggcc cggccccggcg agatcaactgg ctatatggcc accgtacccg 650  
ggctgctgaa ggtgctggag accttcgttg cctgcacatcat cttcgcggtc 700  
atcagcgacc ccaacactgta ccagcaccagg ccggccctgg agtgggtgcgt 750  
ggcggtgtac gccatctgct tcataccttagc ggccatcgcc atcctgctga 800  
acctggggga gtgcaccaac gtgctaccca tcccccctcc cagcttcctg 850  
tcggggctgg ctttgcgtgc tgtcctcctc tatgccaccg cccttgttct 900  
ctggcccttc taccagttcg atgagaagta tggcgccag cctcggcgct 950  
cgagagatgt aagctgcagc cgccagccatg cctactacgt gtgtgcctgg 1000  
gaccgcccac tggctgtggc catcctgacg gccatcaacc tactggcgta 1050  
tgtggctgac ctgggtgcact ctgcccaccc ggtttttgtc aaggctctaag 1100  
actctcccaa gaggctcccg ttccctctcc aacctctttt ttcttcttgc 1150  
ccgagttttc tttatggagt acttctttcc tccgccttcc ctctgtttc 1200  
ctcttcctgt ctccccctccc tcccaccttt ttctttcctt cccaaattcct 1250  
tgcactctaa ccagttcttg gatgcacatctt cttcccttccc ttccctcttg 1300  
ctgtttcctt cctgtgttgt tttgttgcac acatcctgtt ttcacccctg 1350  
agctgtttct ctttttcttt tctttctttt tttttttttt tttaagacg 1400  
gattctcaact ctgtggccca ggctggagtg cagtggtgcg atctcagctc 1450  
actgcaaccc ccgcctcctg ggttcaagcg attctcctcc cccagcctcc 1500  
caagtagctg ggaggacagg tgtgagctgc cgcacccagc ctgtttctct 1550  
ttttccactc ttcttttttc tcatctctt tctgggttgc ctgtcggctt 1600  
tcttatctgc ctgttttgca agcaccttct cctgtgtccct tgggagccct 1650  
gagacttctt tctctcccttg cctccaccca cctccaaagg tgctgagctc 1700  
acatccacac cccttgcagc cgtccatgcc acagcccccc aaggggcccc 1750  
attgccaaag catgcctgcc caccctcgct gtgccttagt cagtgtgtac 1800  
gtgtgtgtgt gtgtgtgttt ggggggtggg ggggtggtag ctggggattt 1850  
ggcccttctt ctccccagtgaa aggaaggtgt gcagtgtact tcccccattaa 1900

attaaaaaac atatatataat atatatttg aggtcagtaa tttccaatgg 1950  
 gcgggaggca ttaagcaccc accctgggtc cctaggcccc gcctggcact 2000  
 cagccctgcc agagattggc tccagaattt ttgccaggt tacagaacac 2050  
 ccactgccta gaggccatct taaaggaagc aggggctgga tgcccttcata 2100  
 cccaaactatt ctctgtggta tgaaaaag 2128

<210> 31 .  
 <211> 322  
 <212> PRT  
 <213> Homo sapiens

<400> 31  
 Met Pro Val Thr Val Thr Arg Thr Thr Ile Thr Thr Thr Thr Thr  
 1 5 10 15

Ser	Ser	Ser	Gly	Leu	Gly	Ser	Pro	Met	Ile	Val	Gly	Ser	Pro	Arg
				20						25				30

Ala	Leu	Thr	Gln	Pro	Leu	Gly	Leu	Leu	Arg	Leu	Leu	Gln	Leu	Val
			35						40					45

Ser	Thr	Cys	Val	Ala	Phe	Ser	Leu	Val	Ala	Ser	Val	Gly	Ala	Trp
			50						55					60

Thr	Gly	Ser	Met	Gly	Asn	Trp	Ser	Met	Phe	Thr	Trp	Cys	Phe	Cys
			65						70					75

Phe	Ser	Val	Thr	Leu	Ile	Ile	Leu	Ile	Val	Glu	Leu	Cys	Gly	Leu
				80					85					90

Gln	Ala	Arg	Phe	Pro	Leu	Ser	Trp	Arg	Asn	Phe	Pro	Ile	Thr	Phe
				95					100					105

Ala	Cys	Tyr	Ala	Ala	Leu	Phe	Cys	Leu	Ser	Ala	Ser	Ile	Ile	Tyr
				110					115					120

Pro	Thr	Thr	Tyr	Val	Gln	Phe	Leu	Ser	His	Gly	Arg	Ser	Arg	Asp
				125					130					135

His	Ala	Ile	Ala	Ala	Thr	Phe	Phe	Ser	Cys	Ile	Ala	Cys	Val	Ala
				140					145					150

Tyr	Ala	Thr	Glu	Val	Ala	Trp	Thr	Arg	Ala	Arg	Pro	Gly	Glu	Ile
				155					160					165

Thr	Gly	Tyr	Met	Ala	Thr	Val	Pro	Gly	Leu	Leu	Lys	Val	Leu	Glu
				170					175					180

Thr	Phe	Val	Ala	Cys	Ile	Ile	Phe	Ala	Phe	Ile	Ser	Asp	Pro	Asn
				185					190					195

Leu	Tyr	Gln	His	Gln	Pro	Ala	Leu	Glu	Trp	Cys	Val	Ala	Val	Tyr
				200					205					210

Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn Leu  
 215 220 225  
 Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu  
 230 235 240  
 Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu  
 245 250 255  
 Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln  
 260 265 270  
 Pro Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr  
 275 280 285  
 Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr  
 290 295 300  
 Ala Ile Asn Leu Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala  
 305 310 315  
 His Leu Val Phe Val Lys Val  
 320

<210> 32  
 <211> 3680  
 <212> DNA  
 <213> Homo sapiens

<400> 32  
 gaacgtgcca ccatgccca ctaattttt tatttttagt agagacgggg 50  
 ttccaccatg ttggccaggc tggcttgaa ctcgtgacct catgatccgc 100  
 tcacctcgcc ctccccaaagt gctgggattt caggcatgag ccactgacgc 150  
 ctggccagcc tatgcatttt taagaaaattt ttctgtatta ggtgctgtgc 200  
 taaacattgg qcactacagt gacaaaaca gactgaattc cccaagagcc 250  
 aaagaccagt gagggagacc aacaagaaac aggaaatgca aaagagacca 300  
 ttattactca ctatgactaa gggtcacaaa tgggtacgt tgatggagag 350  
 tgatttgtta agagactaca gagggaggac agactaccaa gaggggggccc 400  
 agaaaaagctc ctctgacgag gtggatttc agcccaaact ggaagaatga 450  
 gaaagagcta gccagccatc agaatagtcc agaagagatg gggagcacta 500  
 cactcaaac acattggcct gagaaaatag catggattt gaggaggctg 550  
 gggaaacacc acttctgccc acctggccag gaggcattga gggcttgaga 600  
 aagggcaatg gcagtagcag tagaaaggac aggtaggag cagggacttt 650  
 gcaggtggaa tcattaggtc ttatcaacag atatggccaa gcaaagccag 700

gggagaattg atggtaatgc tgaggtttg agccaggcta gatgggacag 750  
 tggtgggtga tgcaaaggaa agaggtcagg aagcagggcc agacgtgggg 800  
 agaaggtgtg ggggttttgt ttccatcttg ccgagtctgc cggaatgtgg 850  
 atgggaagac caagaggagg agcaaggggc agaggggaag ggaatctaa 900  
 agaagtccctg gatgccacac tcttcttcct tcctcctctt ccctctcctc 950  
 agaggtctca ctcgtggttc ttcatttcct gccctgcctc catctcctct 1000  
 gggtgctggg aaagtggagg attagctgaa gtttgcttc tcggggcctg 1050  
 tctgaatctc cattgcttcc tgggaggaca taattcacct gtcctagctt 1100  
 cttatcatct tacatttccc tgttagccact gggacatatg tggtgttcct 1150  
 tcctagctcc tgtctcctcc tcatgcctt gctgggtatg ggcatgttag 1200  
 ggggaaggtc attgctgtca gaggggcact gactttctaa tggtgttacc 1250  
 caaggtgaat gttggagaca cagtcgcgat gctgccaag tcccggcgag 1300  
 ccctaactat ccaggagatc gctgcgctgg ccaggtcctc cctgcatgg 1350  
 atgcagcccc tcccatgttt ctggccactt tgtccttct cctcccgttt 1400  
 gcacatccct ttggaactgt ttcctgtgag tacatgctgg ggtctccct 1450  
 ttcttcctt gtcaggtga atctcagccc cttctccac ccaaagggtc 1500  
 acatggatcc taactactgc caccctcca cctccctgca cctgtgctcc 1550  
 ctggcctggg ctttaccag gttctccac cttcccttat ctccaggtat 1600  
 ttcccaggtg gtgaaggacc acgtgaccaa gcctaccgccc atggcccagg 1650  
 gccgagtggc tcacccatt gagtggagg gctggagcaa gccgagtgac 1700  
 tcacctgctg ccctggaatc agcctttcc tcctattcag acctcagcga 1750  
 gggcgaacaa gaggctcgct ttgcagcagg agtggctgag cagttgcca 1800  
 tcgcggaagc caagctccga gcatggtctt cgggtggatgg cgaggactcc 1850  
 actgatgact cctatgatga ggactttgct gggggatgg acacagacat 1900  
 ggctgggcag ctgcccctgg ggccgcacct ccaggacctg ttcaccggcc 1950  
 accggttctc cggcctgtg cggcagggtc ccgtggagcc tgagagcga 2000  
 tgctcacaga ccgtgtcccc agacaccctg tgctctagtc tgtgcagcct 2050  
 ggaggatggg ttgttggct ccccgcccc gctggctcc cagctgctgg 2100  
 gcgatgagct gcttctcgcc aaactgcccc ccagccggga aagtgcctc 2150

cgcagcctgg gcccactgga ggcccaggac tcactctaca actcgccct 2200  
cacagagtcc tgcctttccc ccgcggagga ggagccagcc ccctgcaagg 2250  
actgccagcc actctgcccc caactaacgg gcagctggga acggcagcgg 2300  
caagcctctg acctggcctc ttctggggtg gtgtccttag atgaggatga 2350  
ggcagagcca gaggaacagt gacccacatc atgcctggca gtggcatgca 2400  
tccccccggct gctgccaggg gcagagcctc tgtgccaag tgtggctca 2450  
aggctcccaag cagagctcca cagcctagag ggctcctggg agcgctcgct 2500  
tctccgttgt gtgtttgca tgaaagtgtt tggagaggag gcaggggctg 2550  
ggctgggggc gcatgtcctg cccccactcc cggggcttc cgggggttgc 2600  
ccggggcctc tggggcatgg ctacagctgt ggcagacagt gatgttcatg 2650  
ttcttaaaat gccacacaca catttcctcc tcggataatg tgaaccacta 2700  
agggggttgt gactgggctg tgtgagggtg ggggtggagg gggcccagca 2750  
accccccacc ctcggccatgc ctctctcttc tctgctttc ttctcacttc 2800  
cgagtccatg tgcagtgcctt gatagaatca ccccccacctg gaggggctgg 2850  
ctcctgcctt cccggagcct atgggtttag ccgtccctca agggccctg 2900  
cccagctggg ctcgtgtgt gcttcattca cctctccatc gtctctaaat 2950  
cttcctcttt tttcctaaag acagaaggtt tttggtctgt ttttcagtc 3000  
ggatcttctc ttctctggga ggcttggaa tgatgaaagc atgtaccctc 3050  
cacccctttc ctggccccct aatggggcct gggcccttcc ccaaccctc 3100  
ctaggatgtg cgggcagtgt gctggcgcct cacagccagc cgggctgccc 3150  
attcacgcag agctctctga gcgggaggtg gaagaaagga tggctctgg 3200  
tgccacagag ctgggacttc atgttcttct agagagggcc acaagagggc 3250  
cacaggggtg gccgggagtt gtcagctgat gcctgctgag aggcaggaat 3300  
tgtgccagtg agtgcacagtc atgagggagt gtctcttctt ggggaggaaa 3350  
gaaggttagag cctttctgtc tgaatgaaag gccaaggcta cagtacaggg 3400  
ccccgccccca gccagggtgt taatgcccac gtagtggagg cctctggcag 3450  
atccctgcatt ccaagggtcac tggactgtac gtttttatgg ttgtggaaag 3500  
ggtgggtggc tttagaatta agggccttgc aggcttggc aggtaaagagg 3550  
gccccaaaggtta agaacgagag ccaacgggca caagcattct atatataagt 3600

ggctcattag gtgttattt tgttctattt aagaatttgt tttatataat 3650  
 taatataaaaa atctttgtaa atctctaaaa 3680  
 <210> 33  
 <211> 335  
 <212> PRT  
 <213> Homo sapiens  
 <400> 33  
 Met Phe Leu Ala Thr Leu Ser Phe Leu Leu Pro Phe Ala His Pro  
     1               5                 10                 15  
 Phe Gly Thr Val Ser Cys Glu Tyr Met Leu Gly Ser Pro Leu Ser  
     20               25                 30  
 Ser Leu Ala Gln Val Asn Leu Ser Pro Phe Ser His Pro Lys Val  
     35               40                 45  
 His Met Asp Pro Asn Tyr Cys His Pro Ser Thr Ser Leu His Leu  
     50               55                 60  
 Cys Ser Leu Ala Trp Ser Phe Thr Arg Leu Leu His Pro Pro Leu  
     65               70                 75  
 Ser Pro Gly Ile Ser Gln Val Val Lys Asp His Val Thr Lys Pro  
     80               85                 90  
 Thr Ala Met Ala Gln Gly Arg Val Ala His Leu Ile Glu Trp Lys  
     95               100                105  
 Gly Trp Ser Lys Pro Ser Asp Ser Pro Ala Ala Leu Glu Ser Ala  
   110               115                120  
 Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala Arg  
   125               130                135  
 Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys  
   140               145                150  
 Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp  
   155               160                165  
 Ser Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala  
   170               175                180  
 Gly Gln Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly  
   185               190                195  
 His Arg Phe Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu  
   200               205                210  
 Ser Asp Cys Ser Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser  
   215               220                225  
 Leu Cys Ser Leu Glu Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu  
   230               235                240

Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro  
 245 250 255  
 Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala  
 260 265 270  
 Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser  
 275 280 285  
 Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu  
 290 295 300  
 Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser  
 305 310 315  
 Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp Glu Asp Glu Ala  
 320 325 330  
 Glu Pro Glu Glu Gln  
 335

<210> 34  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct

<400> 34  
 tgtcctttgt cccagacttc tgtcc 25

<210> 35  
 <211> 50  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-50  
 <223> Synthetic construct.

<400> 35  
 ctggatgcta atgtgtccag taaatgatcc ccttatcccc tcgcgatgct 50

<210> 36  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 36

ttccactcaa tgaggtgagc cactc 25

<210> 37  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 37  
ggcgagccct aactatccag gag 23

<210> 38  
<211> 39  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-39  
<223> Synthetic construct.

<400> 38  
ggagatcgct gcgctggcca ggtcctccct gcatggtat 39

<210> 39  
<211> 22  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-22  
<223> Synthetic construct.

<400> 39  
ctgctgcaaa gcgagcctct tg 22

<210> 40  
<211> 2084  
<212> DNA  
<213> Homo sapiens

<400> 40  
ggtcctggg cgctctgtta cacaaggcaag atacagccag ccccacctaa 50  
ttttgttcc ctggcacccct cctgctcagt ggcacattgt cacacttaac 100  
ccatctgttt tctctaattgc acgacagatt cctttcagac aggacaactg 150  
tgatatttca gttcctgatt gtaaataacct cctaagcctg aagcttctgt 200  
tactagccat tgtgagcttc agtttcttca tctgcaaaat gggcataata 250  
caatctattc ttgccacatc aaggattgt tattccctta aaaaaaaacc 300

aataccaaag aaggctacaa tggtggcctt agccaaaatt ctgttgattt 350  
caacgttgtt ttattcactt ctatcgaaaa gccatggaaa agaaaatcaa 400  
gacataaaaca caacacagaa cattgcagaa gtttttaaaa caatggaaaa 450  
taaacctatt tctttggaaa gtgaagcaaa cttaaactca gataaagaaa 500  
atataaccac ctcaaatttc aaggcgagtc attcccctcc tttgaatcta 550  
cccaacaaca gccacggaat aacagatttc tccagtaact catcagcaga 600  
gcattcttg ggcagtctaa aacccacatc taccattcc acaagccctc 650  
ccttgatcca tagcttggtt tctaaagtgc cttggaatgc acctatagca 700  
gatgaagatc ttttgcacat ctcagcacat cccaatgcta cacctgctct 750  
gtcttcagaa aacttcactt ggtcttgggt caatgacacc gtgaaaactc 800  
ctgataacag ttccattaca gtagcatcc tctcttcaga accaacttct 850  
ccatctgtga cccccctgat agtggAACCA agtggatggc ttaccacaaa 900  
cagtgatagc ttcaactgggt ttaccctta tcaagaaaaa acaactctac 950  
agcctacctt aaaattcacc aataattcaa aactcttcc aaatacgtca 1000  
gatccccaaa aagaaaaatag aaatacagga atagtattcg gggccatttt 1050  
aggtgctatt ctgggtgtct cattgcttac tcttgggc tacttgggt 1100  
gtggaaaaag gaaaacggat tcattttccc atcggcgact ttatgacgac 1150  
agaaatgaac cagttctgcg attagacaat gcaccggAACCTT cttatgatgt 1200  
gagttttggg aattcttagct actacaatcc aactttgaat gattcagcca 1250  
tgccagaaag tgaagaaaat gcacgtgatg gcattcctat ggatgacata 1300  
cctccacttc gtacttctgt atagaactaa cagaaaaag gcgttaaaca 1350  
gcaagtgtca tctacatcct agcctttga caaattcatc tttcaaaagg 1400  
ttacacaaaa ttactgtcac gtggatttttgc tcaaggagaa tcataaaagc 1450  
aggagaccag tagcagaaat gtagacagga tgtatcatcc aaaggtttc 1500  
tttcttacaa ttttggcca tcctgaggca ttacttaagt agccttaatt 1550  
tgtatTTAG tagtattttc ttagtagaaa atattgtgg aatcagataa 1600  
aactaaaaaga ttccaccatt acagccctgc ctcataacta aataataaaa 1650  
attattccac caaaaaattc taaaacaatg aagatgactc ttactgctc 1700  
tgcctgaagc cctagtagcca taattcaaga ttgcattttc ttaaatgaaa 1750

attgaaaggg tgcttttaa agaaaatttg acttaaagct aaaaagagga 1800  
 catagcccag agtttctgtt attggaaat tgaggcaata gaaatgacag 1850  
 acctgtattc tagtacgtta taatttcta gatcagcaca cacatgatca 1900  
 gccccactgag ttatgaagct gacaatgact gcattcaacg gggccatggc 1950  
 aggaaagctg accctaccca ggaaagtaat agcttctta aaagtctca 2000  
 aaggtttgg gaatttaac ttgtcttaat atatcttagg cttcaattat 2050  
 ttgggtgcct taaaaactca atgagaatca tggt 2084

<210> 41  
 <211> 334  
 <212> PRT  
 <213> Homo sapiens

<400> 41  
 Met Leu Ala Leu Ala Lys Ile Leu Leu Ile Ser Thr Leu Phe Tyr  
 1 5 10 15

Ser	Leu	Leu	Ser	Gly	Ser	His	Gly	Lys	Glu	Asn	Gln	Asp	Ile	Asn
20								25					30	

Thr	Thr	Gln	Asn	Ile	Ala	Glu	Val	Phe	Lys	Thr	Met	Glu	Asn	Lys
35								40					45	

Pro	Ile	Ser	Leu	Glu	Ser	Glu	Ala	Asn	Leu	Asn	Ser	Asp	Lys	Glu
50								55					60	

Asn	Ile	Thr	Thr	Ser	Asn	Leu	Lys	Ala	Ser	His	Ser	Pro	Pro	Leu
65								70					75	

Asn	Leu	Pro	Asn	Asn	Ser	His	Gly	Ile	Thr	Asp	Phe	Ser	Ser	Asn
80								85					90	

Ser	Ser	Ala	Glu	His	Ser	Leu	Gly	Ser	Leu	Lys	Pro	Thr	Ser	Thr
95								100					105	

Ile	Ser	Thr	Ser	Pro	Pro	Leu	Ile	His	Ser	Phe	Val	Ser	Lys	Val
110								115					120	

Pro	Trp	Asn	Ala	Pro	Ile	Ala	Asp	Glu	Asp	Leu	Leu	Pro	Ile	Ser
125								130					135	

Ala	His	Pro	Asn	Ala	Thr	Pro	Ala	Leu	Ser	Ser	Glu	Asn	Phe	Thr
140								145					150	

Trp	Ser	Leu	Val	Asn	Asp	Thr	Val	Lys	Thr	Pro	Asp	Asn	Ser	Ser
155								160					165	

Ile	Thr	Val	Ser	Ile	Leu	Ser	Ser	Glu	Pro	Thr	Ser	Pro	Ser	Val
170								175					180	

Thr	Pro	Leu	Ile	Val	Glu	Pro	Ser	Gly	Trp	Leu	Thr	Thr	Asn	Ser
185								190					195	

Asp Ser Phe Thr Gly Phe Thr Pro Tyr Gln Glu Lys Thr Thr Leu  
200 205 210

Gln Pro Thr Leu Lys Phe Thr Asn Asn Ser Lys Leu Phe Pro Asn  
215 220 225

Thr Ser Asp Pro Gln Lys Glu Asn Arg Asn Thr Gly Ile Val Phe  
230 235 240

Gly Ala Ile Leu Gly Ala Ile Leu Gly Val Ser Leu Leu Thr Leu  
245 250 255

Val Gly Tyr Leu Leu Cys Gly Lys Arg Lys Thr Asp Ser Phe Ser  
260 265 270

His Arg Arg Leu Tyr Asp Asp Arg Asn Glu Pro Val Leu Arg Leu  
275 280 285

Asp Asn Ala Pro Glu Pro Tyr Asp Val Ser Phe Gly Asn Ser Ser  
290 295 300

Tyr Tyr Asn Pro Thr Leu Asn Asp Ser Ala Met Pro Glu Ser Glu  
305 310 315

Glu Asn Ala Arg Asp Gly Ile Pro Met Asp Asp Ile Pro Pro Leu  
320 325 330

Arg Thr Ser Val

<210> 42  
<211> 1594  
<212> DNA  
<213> Homo sapiens

<400> 42  
aacaggatct cctcttgcag tctgcagccc aggacgctga ttccagcagc 50  
gccttaccgc gcagccccaa gattcaatat ggtggaaaatc gccttcaata 100  
ccccctaccgc cgtgcaaaaag gaggaggcgc ggcaagacgt ggaggccctc 150  
ctgagccgca cggtcagaac tcagatactg accggcaagg agctccgagt 200  
tgccacccag gaaaaagagg gtcctctgg gagatgtatg cttactctct 250  
taggcctttc attcatcttg gcaggactta ttgttgttgg agcctgcatt 300  
tacaagtact tcatgcccaa gagcaccatt taccgtggag agatgtgctt 350  
tttgattct gaggatcctg caaattccct tcgtggagga gaggctaact 400  
tcctgcctgt gactgaggag gctgacattc gtgaggatga caacattgca 450  
atcattgatg tgcctgtccc cagtttctct gatagtgacc ctgcagcaat 500  
tattcatgac tttgaaaaagg gaatgactgc ttacctggac ttgttgttgg 550

ggaactgcta tctgatgccc ctcaataactt ctattgttat gcctccaaaa 600  
aatctggtag agctcttgg caaactggcg agtggcagat atctgcctca 650  
aacttatgtg gttcgagaag acctagttgc tgtggaggaa attcgtatg 700  
ttagtaacct tggcatctt atttaccaac tttgcaataa cagaaagtcc 750  
ttccgccttc gtcgcagaga cctcttgctg ggttcaaca aacgtgccat 800  
tgataaatgc tggaagatta gacacttccc caacgaattt attgttgaga 850  
ccaagatctg tcaagagtaa gaggcaacag atagagtgtc cttggtaata 900  
agaagtcaga gatttacaat atgactttaa cattaagggtt tatgggatac 950  
tcaagatatt tactcatgca tttactctat tgcttatgct taaaaaaaaag 1000  
aaaaaaaaaa aaaactacta accactgcaa gctcttgtca aatttttagtt 1050  
taattggcat tgcttgaaaa ttgaaactga aattacatga gtttcatttt 1100  
ttctttgcat ttatagggtt tagatttctg aaagcagcat gaatatatca 1150  
cctaacatcc tgacaataaa ttccatccgt tgttttttt gtttgggtt 1200  
tttttctttt ccttaagta agctctttat tcacatctatg gtggagcaat 1250  
tttaaaaattt gaaatatttt aaattgttt tgaactttt gtgtaaaata 1300  
tatcagatct caacattgtt gttttctttt gtttttcatt ttgtacaact 1350  
ttcttgaatt tagaaattac atctttgcag ttctgttagg tgctctgtaa 1400  
ttaacctgac ttatatgtga acaattttca tgagacagtc attttaact 1450  
aatgcagtga ttcttctca ctactatctg tatttgaa tgccacaaaat 1500  
tgtgttaggtg ctgaatgctg taaggagttt aggttgtatg aattctacaa 1550  
ccctataata aattttactc tataaaaaaa aaaaaaaaaa aaaa 1594

<210> 43  
<211> 263  
<212> PRT  
<213> Homo sapiens

<400> 43  
Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu  
1 5 10 15  
Glu Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg  
20 25 30  
Thr Gln Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu  
35 40 45  
Lys Glu Gly Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu

50	55	60
Ser Phe Ile Leu Ala Gly Leu Ile Val Gly	Gly Ala Cys Ile Tyr	
65	70	75
Lys Tyr Phe Met Pro Lys Ser Thr Ile Tyr Arg Gly Glu Met Cys		
80	85	90
Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser	Leu Arg Gly Gly Glu	
95	100	105
Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile Arg Glu Asp		
110	115	120
Asp Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe Ser Asp		
125	130	135
Ser Asp Pro Ala Ala Ile Ile His Asp Phe Glu Lys Gly Met Thr		
140	145	150
Ala Tyr Leu Asp Leu Leu Leu Gly Asn Cys Tyr Leu Met Pro Leu		
155	160	165
Asn Thr Ser Ile Val Met Pro Pro Lys Asn Leu Val Glu Leu Phe		
170	175	180
Gly Lys Leu Ala Ser Gly Arg Tyr Leu Pro Gln Thr Tyr Val Val		
185	190	195
Arg Glu Asp Leu Val Ala Val Glu Glu Ile Arg Asp Val Ser Asn		
200	205	210
Leu Gly Ile Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser Phe		
215	220	225
Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala		
230	235	240
Ile Asp Lys Cys Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile		
245	250	255
Val Glu Thr Lys Ile Cys Gln Glu		
260		

<210> 44  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 44  
gaaagacacg acacagcagc ttgc 24

<210> 45

<211> 20  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-20  
<223> Synthetic construct.

<400> 45  
gggaactgct atctgatgcc 20

<210> 46  
<211> 26  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-26  
<223> Synthetic construct.

<400> 46  
caggatctcc tcttgagtc tgcagc 26

<210> 47  
<211> 28  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-28  
<223> Synthetic construct.

<400> 47  
cttctcgAAC cacataagtt tgaggcag 28

<210> 48  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 48  
cacgattccc tccacagcaa ctggg 25

<210> 49  
<211> 1969  
<212> DNA  
<213> Homo sapiens

<400> 49  
ggaggaggga gggcgggcag gcGCCAGCCC agAGCAGCCC CGGGCACCAg 50

cacggactct ctcttccagc ccaggtgccc cccactctcg ctccattcgg 100  
cgggagcacc cagtccctgta cgccaaggaa ctggtcctgg gggcaccatg 150  
gtttcggcgg cagcccccaag cctcctcatc cttctgttgc tgctgctggg 200  
gtctgtgcct gctaccgacg cccgctctgt gcccctgaag gccacgttcc 250  
tggaggatgt ggccggtagt ggggaggccg agggctcgta ggcctcctcc 300  
ccgagcctcc cgccaccctg gaccccgccc ctcagccca catcgatggg 350  
gcccccagccc acaaccctgg ggggcccata acccccccacc aacttcctgg 400  
atgggatagt ggacttcttc cgccagtacg ttagtgcgtat tgctgtggg 450  
ggctccctgg cctttctgct gatgttcatc gtctgtgccc cggtcatcac 500  
ccggcagaag cagaaggcct cggcctattta cccatcgta ttccccaaga 550  
agaagtacgt ggaccagagt gaccgggccc ggggcccccg ggccttcaagt 600  
gaggtccccg acagagcccc cgacagcagg cccgaggaag ccctggattc 650  
ctcccgccag ctccaggccg acatcttggc cgccaccctg aacctcaagt 700  
ccccccaccag ggctgcactg ggccgtgggg acggagccag gatggtgag 750  
ggcaggggccc cagaggaaga ggagaaggc agccaggagg gggaccagga 800  
agtccaggga catgggtcc cagtggagac accagaggcg caggaggagc 850  
cgtgctcagg ggtccttgag gggctgtgg tggccggta gggccaagg 900  
gagcttggaaag ggtctctttt gttagcccaag gaagcccagg gaccagtggg 950  
tccccccgaa agccctgtg cttgcagcag tgtccacccc agtgtctaacc 1000  
agtccctcccg ggctgcccagc cctgactgtc gggcccccac gtggtcacct 1050  
ccccgtgtat gaaaaggcct tcagccctga ctgcttcctg acactccctc 1100  
cttggcctcc ctgtggtgcc aatcccagca tgtgctgatt ctacagcagg 1150  
cagaaatgct ggtccccgt gccccggagg aatcttacca agtgcacca 1200  
tccttcaccc cagcagcccc aaagggtac atcctacagc acagctcccc 1250  
tgacaaaatgt agggagggca cgtgtccctg tgacagccag gataaaacat 1300  
ccccccaaagt gctgggatta caggcgtgag ccaccgtgcc cggcccaaacc 1350  
tacttttaa aacagctaca gggtaaaatc ctgcagcacc cactctggaa 1400  
aatactgctc ttaattttcc tgaaggtggc cccctgtttc tagttggtcc 1450  
aggatttaggg atgtggggta tagggcattt aaatcccttc aagcgctctc 1500

caagcacccc cgccctgggg gtgagttct catcccgcta ctgctgctgg 1550  
gatcaggttg aatgaatgga actcttcctg tctggcctcc aaagcagcct 1600  
agaagctgag gggctgtgtt tgaggggacc tccaccctgg ggaagtccga 1650  
ggggctgggg aagggtttct gacgcccagc ctggagcagg gggccctgg 1700  
ccacccctg ttgctcacac attgtctggc agcctgtgtc cacaatattc 1750  
gtcagtcctc gacagggagc ctgggctccg tcctgctta gggaggctct 1800  
ggcaggaggt cctctcccc atccctccat ctggggctcc cccaacctct 1850  
gcacagctct ccaggtgctg agatataatg caccagcaca ataaaccttt 1900  
attccggcct gaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 1950  
aaaaaaaaaaa aaaaaaaga 1969

<210> 50  
<211> 283  
<212> PRT  
<213> *Homo sapiens*

```

<400> 50
Met Val Ser Ala Ala Ala Pro Ser Leu Leu Ile Leu Leu Leu Leu
   1           5           10          15

Leu Leu Gly Ser Val Pro Ala Thr Asp Ala Arg Ser Val Pro Leu
   20          25          30

Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu
   35          40          45

Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro
   50          55          60

Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly
   65          70          75

Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe
   80          85          90

Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala
   95         100         105

Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln
  110         115         120

Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys
  125         130         135

Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe
  140         145         150

Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Glu Glu Ala
  155         160         165

```

Leu Asp Ser Ser Arg Gln Leu Gln Ala Asp Ile Leu Ala Ala Thr  
170 175 180

Gln Asn Leu Lys Ser Pro Thr Arg Ala Ala Leu Gly Gly Gly Asp  
185 190 195

Gly Ala Arg Met Val Glu Gly Arg Gly Ala Glu Glu Glu Glu Lys  
200 205 210

Gly Ser Gln Glu Gly Asp Gln Glu Val Gln Gly His Gly Val Pro  
215 220 225

Val Glu Thr Pro Glu Ala Gln Glu Glu Pro Cys Ser Gly Val Leu  
230 235 240

Glu Gly Ala Val Val Ala Gly Glu Gly Gln Gly Glu Leu Glu Gly  
245 250 255

Ser Leu Leu Leu Ala Gln Glu Ala Gln Gly Pro Val Gly Pro Pro  
260 265 270

Glu Ser Pro Cys Ala Cys Ser Ser Val His Pro Ser Val  
275 280

<210> 51  
<211> 1734  
<212> DNA  
<213> Homo sapiens

<400> 51  
gtggactctg agaagccag gcagttgagg acaggagaga gaaggctgca 50  
gacccagagg gagggaggac agggagtcgg aaggaggagg acagaggagg 100  
gcacagagac gcagagcaag ggcggcaagg aggagaccct ggtgggagga 150  
agacactctg gagagagagg gggctggca gagatgaagt tccaggggcc 200  
cctggcctgc ctcctgctgg ccctctgcct gggcagtggg gaggctggcc 250  
ccctgcagag cggagaggaa agcactggga caaatattgg ggaggccctt 300  
ggacatggcc tgggagacgc cctgagcgaa ggggtggaa aggccattgg 350  
caaagaggcc ggagggcag ctggctctaa agtcagttag gcccattggcc 400  
aagggaccag agaagcagtt ggcactggag tcaggcaggt tccaggctt 450  
ggcgcagcag atgcttggg caacagggtc gggaaagcag cccatgctct 500  
ggaaaacact gggcacgaga ttggcagaca ggcagaagat gtcattcgac 550  
acggagcaga tgctgtccgc ggctcctggc aggggtggcc tggccacagt 600  
ggtgcttggg aaacttctgg aggccatggc atcttggct ctaaggtgg 650  
ccttggagggc cagggccagg gcaatcctgg aggtctgggg actccgtggg 700

tccacggata cccccgaaac tcagcaggca gcttggaaat gaatcctcag 750  
ggagctccct ggggtcaagg aggcaatggaa gggccaccaa actttggac 800  
caacactcag ggagctgtgg cccagcctgg ctatggttca gtgagagcca 850  
gcaaccagaa tgaagggtgc acgaatcccc caccatctgg ctcaggtgga 900  
ggctccagca actctggggg aggcaagcggc tcacagtcgg gcagcagtgg 950  
cagtggcagc aatggtgaca acaacaatgg cagcagcagt ggtggcagca 1000  
gcagtggcag cagcagtggc agcagcagtgc gcggcagcag tggcggcagc 1050  
agtggtgca gcagtggcaa cagtggtggc agcagaggtg acagcggcag 1100  
ttagtcctcc tgggatcca gcaccggctc ctccctccggc aaccacggtg 1150  
ggagcggcgg agaaatggaa cataaaccgg ggtgtgaaaa gccaggaaat 1200  
gaagcccgcg ggagcggggaa atctggatt caggcattca gaggacaggg 1250  
agtttccagc aacatgaggg aaataagcaa agagggcaat cgcctccttg 1300  
gaggctctgg agacaattat cggggcaag ggtcgagctg gggcagtgg 1350  
ggaggtgacg ctgttgggg agtcaatact gtgaactctg agacgtctcc 1400  
tggatgttt aactttgaca ctttctggaa gaattttaaa tccaagctgg 1450  
gtttcatcaa ctggatgcc ataaacaagg accagagaag ctctcgcatc 1500  
ccgtgacctc cagacaagga gccaccagat tggatggag ccccccacact 1550  
ccctccttaa aacaccaccc tctcatcaact aatctcagcc cttgccttg 1600  
aaataaacct tagctgcccc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1700  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1734

<210> 52  
<211> 440  
<212> PRT  
<213> Homo sapiens

<400> 52  
Met Lys Phe Gln Gly Pro Leu Ala Cys Leu Leu Leu Ala Leu Cys  
1 5 10 15  
Leu Gly Ser Gly Glu Ala Gly Pro Leu Gln Ser Gly Glu Glu Ser  
20 25 30  
Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp  
35 40 45  
Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly

	50		55		60
Gly Ala Ala Gly Ser Lys Val Ser Glu Ala Leu Gly Gln Gly Thr					
65			70		75
Arg Glu Ala Val Gly Thr Gly Val Arg Gln Val Pro Gly Phe Gly					
80			85		90
Ala Ala Asp Ala Leu Gly Asn Arg Val Gly Glu Ala Ala His Ala					
95			100		105
Leu Gly Asn Thr Gly His Glu Ile Gly Arg Gln Ala Glu Asp Val					
110			115		120
Ile Arg His Gly Ala Asp Ala Val Arg Gly Ser Trp Gln Gly Val					
125			130		135
Pro Gly His Ser Gly Ala Trp Glu Thr Ser Gly Gly His Gly Ile					
140			145		150
Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln Gly Gln Gly Asn Pro					
155			160		165
Gly Gly Leu Gly Thr Pro Trp Val His Gly Tyr Pro Gly Asn Ser					
170			175		180
Ala Gly Ser Phe Gly Met Asn Pro Gln Gly Ala Pro Trp Gly Gln					
185			190		195
Gly Gly Asn Gly Gly Pro Pro Asn Phe Gly Thr Asn Thr Gln Gly					
200			205		210
Ala Val Ala Gln Pro Gly Tyr Gly Ser Val Arg Ala Ser Asn Gln					
215			220		225
Asn Glu Gly Cys Thr Asn Pro Pro Pro Ser Gly Ser Gly Gly Gly					
230			235		240
Ser Ser Asn Ser Gly Gly Ser Gly Ser Gln Ser Gly Ser Ser					
245			250		255
Gly Ser Gly Ser Asn Gly Asp Asn Asn Asn Gly Ser Ser Ser Gly					
260			265		270
Gly Ser Ser Ser Gly Ser Ser Ser Gly Ser Ser Ser Gly Gly Ser					
275			280		285
Ser Gly Gly Ser Ser Gly Ser Ser Gly Asn Ser Gly Gly Ser					
290			295		300
Arg Gly Asp Ser Gly Ser Glu Ser Ser Trp Gly Ser Ser Thr Gly					
305			310		315
Ser Ser Ser Gly Asn His Gly Gly Ser Gly Gly Asn Gly His					
320			325		330
Lys Pro Gly Cys Glu Lys Pro Gly Asn Glu Ala Arg Gly Ser Gly					
335			340		345

Glu Ser Gly Ile Gln Gly Phe Arg Gly Gln Gly Val Ser Ser Asn  
350 355 360  
Met Arg Glu Ile Ser Lys Glu Gly Asn Arg Leu Leu Gly Gly Ser  
365 370 375  
Gly Asp Asn Tyr Arg Gly Gln Gly Ser Ser Trp Gly Ser Gly Gly  
380 385 390  
Gly Asp Ala Val Gly Gly Val Asn Thr Val Asn Ser Glu Thr Ser  
395 400 405  
Pro Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser  
410 415 420  
Lys Leu Gly Phe Ile Asn Trp Asp Ala Ile Asn Lys Asp Gln Arg  
425 430 435  
Ser Ser Arg Ile Pro  
440

<210> 53  
<211> 3580  
<212> DNA  
<213> Homo sapiens

<400> 53  
gaccgggtccc tccgggcctg gatgtgcgga ctctgctgca gcgagggctg 50  
caggccccgcc gggcggtgct caccgtgccc tggctggtgg agtttctctc 100  
ctttgctgac catgttgttc ctttgctgga atattaccgg gacatcttca 150  
ctctcctgct gcgcctgcac cggagcttgg tggctgcga ggagagttag 200  
ggaaagatgt gtttcctgaa caagctgctg ctacttgctg tcctgggctg 250  
gcttttccag attcccacag tccctgagga cttgttctt ctggaagagg 300  
gtccctcata tgcctttgag gtggacacag tagccccaga gcatggctt 350  
gacaatgcgc ctgtggtgga ccagcagctg ctctacacacct gctgccccta 400  
catcgagag ctccggaaac tgctcgcttc gtgggtgtca ggcagtagtg 450  
gacggagtg 500  
ctgggagccc agccttcca gaccagccag gggctgcagg cacagctcgc 550  
ccaggcctt ttccacaacc agccgcctc cttgcgcggg accgttagtg 600  
tcgtggcaga aagaattgga tcaaactgtg tcaaacatat caaggctaca 650  
ctgggtggcag atctggtgcg ccaggcagag tcacttctcc aagagcagct 700  
ggtgacacag ggagaggaag ggggagaccc agcccagctg ttggagatct 750  
tgtgttccca gctgtgcct cacggggccc aggcattggc cctggggcgg 800

gagttctgtc aaaggaagag ccctgggct gtgcggcgc tgcttccaga 850  
ggagaccccg gcagccgttc tgagcagtgc agagaacatt gctgtgggc 900  
ttgcaacaga gaaaggctgt gcttggctgt cagccaacat cacagcactg 950  
atcaggaggg aggtgaaagc agcagtgagt cgcacacttc gagcccaggg 1000  
tcctgaacct gctgcccggg gggagcggag gggctgctcc cgccctgac 1050  
gtgctctcct tggccgtggg gccacgggac cctgacgagg gagtctcccc 1100  
agagcatctg gaacagctcc taggccagct gggccagacg ctgcggtgcc 1150  
gccagttcct gtgcccacct gctgagcagc atctggcaa gtgctctgtg 1200  
gagtttagctt ccctcctcgt tgcagatcaa attcctatcc tagggcccc 1250  
ggcacagtac aggctggaga gagggcaggg tcgaaggctt ctgcacatgc 1300  
tgcttcctt gtggaaggaa gactttcagg ggccggttcc gtcagcgtg 1350  
ctgctgagcc caagaaatgt ggggcttctg gcagacacaa ggccaaggga 1400  
gtgggacttg ctgctattct tgctacggg gctggtggag aagggtctga 1450  
tgggacggat ggagatagag gcctgcctgg gcagcctcca ccaggcccag 1500  
tggccagggg actttgctga agaattagca acactgtcta atctgttct 1550  
agccgagccc cacctgccag aaccccagct aagagcctgt gagttggtgc 1600  
agccaaaccg gggcaactgtg ctggcccaga gctagggtcg agaagtggcc 1650  
ctgccttggg cattgcacca gaaccttggc ccccccctc acgaggagggc 1700  
ccaagtgccc aatgcagacc ctcactgggt ggggtgttagc tgggtctaca 1750  
gtcagacttc ctgctctaag ggtgtcactg cctggcatcc caccacgcga 1800  
atcctagagg aaggagagtt ggcctgattt gggattatgg cagaaaagtc 1850  
cagagatgcc agtcctggag tagaagaggt ggtgtttgtt tatctcttgg 1900  
atactaaatg aaatgaggtg tgtggcttg tcaacacaga attcaagcct 1950  
catttgctat cccagcatct cttaaaaactt tgttgtcttga gaattcatga 2000  
cagaggcaaa tgactcctgc ttaacttatg aagaaaagtta aaacatgaat 2050  
cttgggagtc tacattttct tatcaccagg agctggactg ccatctcctt 2100  
ataaaatgcct aacacaggcc gggctgggtg gtcctgcct gtaatcccag 2150  
cactttgaga ggcctgaggt cggcggactg cctgaggtca ggaattcaag 2200  
accagcctgg ccaacatggc aaaaccccat ctctactaaa aataaaaaaa 2250

ttattagctg ggcatggtgg tgtgtgcctg taatcccagc tactcaggag 2300  
gatgaggcag gagacacctgct tgaacctgga ggtggagggt gcagtgagcc 2350  
gaggtcgcac cactgcactc cagtctgggt aacagagcga gactttctag 2400  
aaaaagccta acaaacagat aaggttaggac tcaaccaact gaaacctgac 2450  
tttccccctg taccttcagc ccctgtgcag gtagtaacct cttgagacct 2500  
ctccctgacc agggaccaag cacagggcat ttagagcttt ttagaataaa 2550  
ctggttttct ttaaaaaaaaaaaaaaaaaa agggcggccg ccctttttt 2600  
ttttttttt ttttttttt ttttttttt ttttttttt taaaaaggc 2650  
ttttattaaa attctccccca cacgatggct cctgcaatct gccacagctc 2700  
tggggcgtgt cctgtaggaa aaggccctgt tttccctgag gcggggctgg 2750  
gcttgtccat gggtccgcgg agctggccgt gcttggcgcc ctggcgtgtg 2800  
tctagctgct tcttgcggg cacagagctg cggggctgg gggcaccggg 2850  
agctaagagc aggctctggt gcaggggtgg aggcctgtct cttaaccgac 2900  
accctgaggt gctcctgaga tgctgggtcc accctgagtg gcacggggag 2950  
cagctgtggc cggtgctcct tcyclaggcca gtcctggga aactaagctc 3000  
gggcccttct ttgcaaagac cgaggatggg gtgggtgtgg gggactcatg 3050  
gggaatggcc tgaggagcta cgtgtgaaga gggcgccggg ttgttggctg 3100  
cagcggcctg gagcgcctct ctcctgagcc tcagtttccc tttccgtcta 3150  
atgaagaaca tgccgtctcg gtgtctcagg gctattagga cttgcctca 3200  
ggaagtggcc ttggacgagc gtcatgttat tttcacaact gtcctgcgac 3250  
gttggcctgg gcacgtcatg gaatggccca tgcctctg ctgcgtggac 3300  
gtcgcggctcg ggagtgcgca gccagaggcg gggccagacg tgcgcctggg 3350  
ggtgagggga ggcgcggccgg gagggcctca caggaagttt ggctcccgca 3400  
ccaccaggca gggcgggctc cccgcggccgc cggccggccacc accgtccagg 3450  
ggccggtaga caaatggaa gtcgcgtttt ggctcgctgc gcagcaggta 3500  
gcccttgcgtat cagtgcggca ggcgcgtcgca cggccaggctgg aagcagcggcc 3550  
cgtccaccag cacgaacagc cgggtgcgcct 3580

<210> 54  
<211> 280  
<212> PRT  
<213> Homo sapiens

<400> 54  
 Met Cys Phe Leu Asn Lys Leu Leu Leu Ala Val Leu Gly Trp  
 1 5 10 15  
 Leu Phe Gln Ile Pro Thr Val Pro Glu Asp Leu Phe Phe Leu Glu  
 20 25 30  
 Glu Gly Pro Ser Tyr Ala Phe Glu Val Asp Thr Val Ala Pro Glu  
 35 40 45  
 His Gly Leu Asp Asn Ala Pro Val Val Asp Gln Gln Leu Leu Tyr  
 50 55 60  
 Thr Cys Cys Pro Tyr Ile Gly Glu Leu Arg Lys Leu Leu Ala Ser  
 65 70 75  
 Trp Val Ser Gly Ser Ser Gly Arg Ser Gly Gly Phe Met Arg Lys  
 80 85 90  
 Ile Thr Pro Thr Thr Ser Leu Gly Ala Gln Pro Ser Gln  
 95 100 105  
 Thr Ser Gln Gly Leu Gln Ala Gln Leu Ala Gln Ala Phe Phe His  
 110 115 120  
 Asn Gln Pro Pro Ser Leu Arg Arg Thr Val Glu Phe Val Ala Glu  
 125 130 135  
 Arg Ile Gly Ser Asn Cys Val Lys His Ile Lys Ala Thr Leu Val  
 140 145 150  
 Ala Asp Leu Val Arg Gln Ala Glu Ser Leu Leu Gln Glu Gln Leu  
 155 160 165  
 Val Thr Gln Gly Glu Glu Gly Gly Asp Pro Ala Gln Leu Leu Glu  
 170 175 180  
 Ile Leu Cys Ser Gln Leu Cys Pro His Gly Ala Gln Ala Leu Ala  
 185 190 195  
 Leu Gly Arg Glu Phe Cys Gln Arg Lys Ser Pro Gly Ala Val Arg  
 200 205 210  
 Ala Leu Leu Pro Glu Glu Thr Pro Ala Ala Val Leu Ser Ser Ala  
 215 220 225  
 Glu Asn Ile Ala Val Gly Leu Ala Thr Glu Lys Ala Cys Ala Trp  
 230 235 240  
 Leu Ser Ala Asn Ile Thr Ala Leu Ile Arg Arg Glu Val Lys Ala  
 245 250 255  
 Ala Val Ser Arg Thr Leu Arg Ala Gln Gly Pro Glu Pro Ala Ala  
 260 265 270  
 Arg Gly Glu Arg Arg Gly Cys Ser Arg Ala  
 275 280

<210> 55  
<211> 2401  
<212> DNA  
<213> Homo sapiens

<400> 55  
tcccttgaca ggtctggtgg ctgggtcggg gtctactgaa ggctgtctt 50  
atcaggaaac tgaagactct ctgctttgc cacagcagtt cctgcagctt 100  
ccttgaggtg tgaacccaca tccctgcccc cagggccacc tgcaggacgc 150  
cgacacacctac ccctcagcag acgcccggaga gaaatgagta gcaacaaaga 200  
gcagcggtca gcagtgttcg tgatcctt tgcctcatc accatcctca 250  
tcctctacag ctccaacagt gccaatgagg tcttccatta cggctccctg 300  
cggggccgta gccgccgacc tgtcaacctc aagaagtgga gcatcactga 350  
cggttatgtc cccattctcg gcaacaagac actgccctct cgggccacc 400  
agtgtgtgat tgtcagcagc tccagccacc tgctggcac caagctggc 450  
cctgagatcg agcgggctga gtgtacaatc cgcatgaatg atgcacccac 500  
cactggctac tcagctgatg tggcaacaa gaccacctac cgcgtcgtgg 550  
cccattccag tgtgttccgc gtgctgagga ggccccagga gtttgtcaac 600  
cggacccctg aaaccgtgtt catttctgg gggcccccga gcaagatgca 650  
gaagccccag ggcagcctcg tgcgtgtgat ccagcgagcg ggcctggtgt 700  
tcccccaacat ggaagcatat gccgtctctc ccggccgcat gcgcaattt 750  
gacgacctct tccgggtga gacggcaag gacagggaga agtctcattc 800  
gtgggtgagc acaggctggt ttaccatggt gatcgccgtg gagttgtgtg 850  
accacgtgca tgtctatggc atggtcccc ccaactactg cagccagcgg 900  
ccccgcctcc agcgcatgcc ctaccactac tacgagccca aggggcccgg 950  
cgaatgtgtc acctacatcc agaatgagca cagtcgcaag ggcaaccacc 1000  
accgcttcat caccgagaaa agggtcttct catcggtggc ccagctgttat 1050  
ggcatcacct tctcccaccc ctccctggacc taggccaccc agcctgtggg 1100  
acctcaggag ggtcagagga gaagcagcct ccgcccagcc gctaggccag 1150  
ggaccatctt ctggccaatc aaggcttgct ggagtgtctc ccagccaaatc 1200  
agggccttga ggaggatgta tcctccagcc aatcagggcc tggggaatct 1250  
gttggcgaat cagggatttg ggagtctatg tggtaatca ggggtgtctt 1300

tcttgtcag tcagggtctg cgcacagtca atcaggtag aggggtatt 1350  
tctgagtcaa tctgaggcta aggacatgtc cttccatg aggccttggt 1400  
tcagagcccc aggaatggac ccccaatca ctccccactc tgctggata 1450  
atggggtcct gtcccaagga gctggaaact tggtgttgc ccctcaattt 1500  
ccagcaccag aaagagagat tgtgtgggg tagaagctgt ctggaggccc 1550  
ggccagagaa tttgtgggt tggaggtt gtggggcggt ggggaggtc 1600  
ccagaggtgg gaggctggca tccaggtctt ggctctgccc tgagacctt 1650  
gacaaaccct tcccccttc tggcaccct tctgcccaca ccagttcca 1700  
gtgcggagtc tgagaccctt tccacccccc ctacaagtgc cctcggtct 1750  
gtcctcccg tctggaccct cccagccact atcccttgct ggaaggctca 1800  
gctctttggg gggctgggg tgacctcccc acctcctgga aaactttagg 1850  
gtattttgc gcaaactcct tcagggttgg gggactctga aggaaacggg 1900  
acaaaacctt aagctgtttt cttagccct cagccagctg ccattagctt 1950  
ggctcttaaa gggccaggcc tcctttctg ccctctagca gggaggttt 2000  
ccaactgttg gaggcgcctt tgggctgcc ccttgcgtc gagtcactgg 2050  
gggcttccga gggctccct cgaccctctg tcgtcctggg atggctgtcg 2100  
ggagctgtat cacctgggtt ctgtccctg gctctgtatc aggcaactta 2150  
ttaaagctgg gcctcagtgg ggtgttttgc tctcctgctc ttctggagcc 2200  
tggaaaggaaa gggcttcagg aggaggctgt gaggctggag ggaccagatg 2250  
gaggaggcca gcagctagcc attgcacact ggggtgatgg gtggggcggt 2300  
tgactgcccc agacttggtt ttgtaatgtat ttgtacagga ataaacacac 2350  
ctacgctccg gaaaaaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 2400  
a 2401

<210> 56  
<211> 299  
<212> PRT  
<213> Homo sapiens

<400> 56  
Met Ser Ser Asn Lys Glu Gln Arg Ser Ala Val Phe Val Ile Leu  
1 5 10 15  
Phe Ala Leu Ile Thr Ile Leu Ile Tyr Ser Ser Asn Ser Ala  
20 25 30

Asn	Glu	Val	Phe	His	Tyr	Gly	Ser	Leu	Arg	Gly	Arg	Ser	Arg	Arg
				35				40					45	
Pro	Val	Asn	Leu	Lys	Lys	Trp	Ser	Ile	Thr	Asp	Gly	Tyr	Val	Pro
				50				55					60	
Ile	Leu	Gly	Asn	Lys	Thr	Leu	Pro	Ser	Arg	Cys	His	Gln	Cys	Val
				65				70					75	
Ile	Val	Ser	Ser	Ser	Ser	His	Leu	Leu	Gly	Thr	Lys	Leu	Gly	Pro
				80				85					90	
Glu	Ile	Glu	Arg	Ala	Glu	Cys	Thr	Ile	Arg	Met	Asn	Asp	Ala	Pro
				95				100					105	
Thr	Thr	Gly	Tyr	Ser	Ala	Asp	Val	Gly	Asn	Lys	Thr	Thr	Tyr	Arg
				110				115					120	
Val	Val	Ala	His	Ser	Ser	Val	Phe	Arg	Val	Leu	Arg	Arg	Pro	Gln
				125				130					135	
Glu	Phe	Val	Asn	Arg	Thr	Pro	Glu	Thr	Val	Phe	Ile	Phe	Trp	Gly
				140				145					150	
Pro	Pro	Ser	Lys	Met	Gln	Lys	Pro	Gln	Gly	Ser	Leu	Val	Arg	Val
				155				160					165	
Ile	Gln	Arg	Ala	Gly	Leu	Val	Phe	Pro	Asn	Met	Glu	Ala	Tyr	Ala
				170				175					180	
Val	Ser	Pro	Gly	Arg	Met	Arg	Gln	Phe	Asp	Asp	Leu	Phe	Arg	Gly
				185				190					195	
Glu	Thr	Gly	Lys	Asp	Arg	Glu	Lys	Ser	His	Ser	Trp	Leu	Ser	Thr
				200				205					210	
Gly	Trp	Phe	Thr	Met	Val	Ile	Ala	Val	Glu	Leu	Cys	Asp	His	Val
				215				220					225	
His	Val	Tyr	Gly	Met	Val	Pro	Pro	Asn	Tyr	Cys	Ser	Gln	Arg	Pro
				230				235					240	
Arg	Leu	Gln	Arg	Met	Pro	Tyr	His	Tyr	Tyr	Glu	Pro	Lys	Gly	Pro
				245				250					255	
Asp	Glu	Cys	Val	Thr	Tyr	Ile	Gln	Asn	Glu	His	Ser	Arg	Lys	Gly
				260				265					270	
Asn	His	His	Arg	Phe	Ile	Thr	Glu	Lys	Arg	Val	Phe	Ser	Ser	Trp
				275				280					285	
Ala	Gln	Leu	Tyr	Gly	Ile	Thr	Phe	Ser	His	Pro	Ser	Trp	Thr	
				290				295						

<210> 57  
 <211> 4277  
 <212> DNA  
 <213> Homo sapiens

<400> 57  
gtttctcata gttggcgctct tctaaaggaa aaacactaaa atgaggaact 50  
cagcggaccg ggagcgacgc agcttgagg aagcatccct agctgttggc 100  
gcagaggggc gaggctgaag ccgagtggcc cgaggtgtct gaggggctgg 150  
ggcaaaggtaa aaagagtttc agaacaagct tcctggaacc catgaccat 200  
gaagtcttgt cgacatttat accgtctgag gtagcagct cgaaactaga 250  
agaagtggag tggccagg gacggcagta tctcttgc tgaccctggc 300  
ggctatggg acgtggctt cagaccccttgc tgatacacca tgctgcgtgg 350  
gacgatgacg gcgtggagag gaatgaggcc tgaggtcaca ctggcttgcc 400  
tcctcctagc cacagcaggc tgctttgctg acttgaacga ggtccctcag 450  
gtcaccgtcc agcctgcgtc caccgtccag aagccggag gcactgtgat 500  
cttgggctgc gtggtaaac ctccaaggat gaatgttaacc tggcgcctga 550  
atggaaagga gctgaatggc tcggatgatg ctctgggtgt cctcatcacc 600  
cacgggaccc tcgtcatcac tgcccttaac aaccacactg tgggacggta 650  
ccagtgtgtg gcccggatgc ctgcggggc tgtggccagc gtgccagcca 700  
ctgtgacact agccaatctc caggacttca agttagatgt gcagcacgtg 750  
attgaagtgg atgagggaaa cacagcagtc attgcctgcc acctgcctga 800  
gagccacccc aaagcccagg tccggatcag cgtcaaacaa gagtggctgg 850  
aggcctccag aggttaactac ctgatcatgc cctcaggaa cctccagatt 900  
gtgaatgcca gccaggagga cgagggcatg tacaagtgtg cagcctacaa 950  
cccagtgacc caggaagtga aaacctccgg ctccagcgcac aggctacgtg 1000  
tgcggcgtc caccgtgag gctgcccgc tcatctaccc cccagaggcc 1050  
caaaccatca tcgtcaccaa aggccagagt ctcatctgg agtgtgtggc 1100  
cagtggaaatc ccaccccccac gggtcacctg gccaaggat gggtccagtg 1150  
tcaccggcta caacaagacg cgcttcctgc tgagcaacct cctcatcgac 1200  
accaccagcg aggaggactc aggcacctac cgctgcattgg ccgacaatgg 1250  
ggttgggcag cccggggcag cggtcacccct ctacaatgtc caggtgtttg 1300  
aacccctga ggtcaccatg gagctatccc agctggcat cccctggggc 1350  
cagagtgcca agcttacctg tgaggtgcgt gggaaacccc cgcctccgt 1400  
gctgtggctg aggaatgctg tgccctcat ctccagccag cgcctccggc 1450

tctcccgca ggcctgcgc gtgctcagca tggggcctga ggacgaaggc 1500  
gtctaccagt gcatggccga gaacgaggtt gggagcgccc atgccgtagt 1550  
ccagctgcgg acctccaggc caagcataac cccaaggcta tggcaggatg 1600  
ctgagctggc tactggcaca cctcctgtat caccctccaa actcggcaac 1650  
cctgagcaga tgctgagggg gcaaccggcg ctccccagac ccccaacgtc 1700  
agtggggcct gcttccccga agtgtccagg agagaagggg cagggggctc 1750  
ccgcccgggc tccccatcatc cttagctcgc cccgcacccctc caagacagac 1800  
tcatatgaac tggtgtggcg gcctcggcat gagggcagtg gccgggcgcc 1850  
aatcctctac tatgtggta aacaccgcaa gcaggtcaca aattcctctg 1900  
acgattggac catctctggc attccagcca accagcacccg cctgaccctc 1950  
accagacttg accccgggag cttgtatgaa gtggagatgg cagcttacaa 2000  
ctgtgcggga gagggccaga cagccatggt cacctccga actggacggc 2050  
ggcccaaacc cgagatcatg gccagcaaag agcagcagat ccagagagac 2100  
gaccctggag ccagtcggca gaggcagcgc cagccagacc acggccgcct 2150  
ctccccccca gaagctcccg acaggcccac catctccacg gcctccgaga 2200  
cctcagtgtt cgtgacactgg attccccgtg ggaatggtgg gttcccaatc 2250  
cagtccttcc gtgtggagta caagaagcta aagaaagtgg gagactggat 2300  
tctggccacc agcgccatcc ccccatcgcg gctgtccgtg gagatcacgg 2350  
gcctagagaa aggacacctcc tacaagttt gactccggc tctgaacatg 2400  
ctgggggaga gcgagcccg cgccccctct cggccctacg tgggtgcgg 2450  
ctacagcggt cgcgtgtacg agaggcccg ggcaggtcct tatatcacct 2500  
tcacggatgc ggtcaatgag accaccatca tgctcaagtg gatgtacatc 2550  
ccagcaagta acaacaacac cccaaatccat ggctttata tctattatcg 2600  
acccacagac agtgacaatg atagtgacta caagaaggat atggtgaaag 2650  
gggacaagta ctggcactcc atcagccacc tgcagccaga gacccctac 2700  
gacattaaga tgcagtgcctt caatgaaggaa ggggagagcg agttcagcaa 2750  
cgtgatgatc tgtgagacca aagctcggaa gtcttctggc cagcctggc 2800  
gactgccacc cccaaactctg gccccaccac agccgccccct tcctgaaacc 2850  
atagagcgcc cggtggcac tggggccatg gtggctcgct ccagcgacct 2900

gccctatctg attgtcgaaa tcgtcctggg ctccatcgaa ctcacatcatcg 2950  
tcacccatccc ttgtggaggg cctggctaa gcaaaaacat 3000  
acaacagacc tgggtttcc tcgaagtgc cttccaccct cctgccccgt 3050  
tactatggtg ccattggag gactcccagg ccaccaggcc agtggacagc 3100  
cctacccatcgat tggcatcagt ggacgggcgt gtgctaattgg gatccacatg 3150  
aataggggct gcccctcgcc tgcagtggc taccggca tgaagcccc 3200  
gcagcactgc ccaggcgagc ttcaagcagca gagtgacacc agcagcctgc 3250  
tgaggcagac ccatcttggc aatggatatg acccccaaag tcaccagatc 3300  
acgaggggtc ccaagtcttag cccggacgag ggctctttct tatacacact 3350  
gccccgacgac tccactcacc agctgctgca gccccatcac gactgctgcc 3400  
aacgcccagga gcagcctgct gctgtggcc agtcaggggt gaggagagcc 3450  
cccgacagtc ctgtcctgga agcagtgtgg gaccctccat ttcaactcagg 3500  
gccccatgc tgcttggcc ttgtgccagt tgaagaggtg gacagtcctg 3550  
actcctgcca agtgagtgga ggagactgggt gtccccagca ccccgtaggg 3600  
gcctacgttag gacaggaacc tggaaatgcag ctctccccgg ggccactggt 3650  
gcgtgtgtct tttgaaacac cacctctcac aatttaggca gaagctgata 3700  
tcccagaaag actatatatt gttttttttt taaaaaaaaa agaagaaaaaa 3750  
agagacagag aaaattggta ttatattttc tattatagcc atatttatat 3800  
atttatgcac ttgtaaataa atgtatatgt tttataattc tggagagaca 3850  
taaggagtcc tacccgttga ggttggagag ggaaaaataaa gaagctgcca 3900  
cctaacagga gtcacccagg aaagcaccgc acaggctggc gcgggacaga 3950  
ctcctaacct ggggcctctg cagtggcagg cgaggctgca ggaggccac 4000  
agataagctg gcaagaggaa ggatcccagg cacatggttc atcacgagca 4050  
tgagggaaaca gcaagggca cggtatcaca gcctggagac acccacacag 4100  
atggctggat ccggctgctac gggaaacatt ttccctaaat gccccatgaga 4150  
acagaccaag atgtgtacag cactatgagc attaaaaaac cttccagaat 4200  
caataatccg tggcaacata tctctgtaaa aacaaacact gtaacttcta 4250  
aataaatgtt tagtcttccc tgtaaaa 4277

<210> 58  
<211> 1115

<212> PRT  
<213> Homo sapiens

<400> 58  
Met Leu Arg Gly Thr Met Thr Ala Trp Arg Gly Met Arg Pro Glu  
1 5 10 15  
Val Thr Leu Ala Cys Leu Leu Leu Ala Thr Ala Gly Cys Phe Ala  
20 25 30  
Asp Leu Asn Glu Val Pro Gln Val Thr Val Gln Pro Ala Ser Thr  
35 40 45  
Val Gln Lys Pro Gly Gly Thr Val Ile Leu Gly Cys Val Val Glu  
50 55 60  
Pro Pro Arg Met Asn Val Thr Trp Arg Leu Asn Gly Lys Glu Leu  
65 70 75  
Asn Gly Ser Asp Asp Ala Leu Gly Val Leu Ile Thr His Gly Thr  
80 85 90  
Leu Val Ile Thr Ala Leu Asn Asn His Thr Val Gly Arg Tyr Gln  
95 100 105  
Cys Val Ala Arg Met Pro Ala Gly Ala Val Ala Ser Val Pro Ala  
110 115 120  
Thr Val Thr Leu Ala Asn Leu Gln Asp Phe Lys Leu Asp Val Gln  
125 130 135  
His Val Ile Glu Val Asp Glu Gly Asn Thr Ala Val Ile Ala Cys  
140 145 150  
His Leu Pro Glu Ser His Pro Lys Ala Gln Val Arg Tyr Ser Val  
155 160 165  
Lys Gln Glu Trp Leu Glu Ala Ser Arg Gly Asn Tyr Leu Ile Met  
170 175 180  
Pro Ser Gly Asn Leu Gln Ile Val Asn Ala Ser Gln Glu Asp Glu  
185 190 195  
Gly Met Tyr Lys Cys Ala Ala Tyr Asn Pro Val Thr Gln Glu Val  
200 205 210  
Lys Thr Ser Gly Ser Ser Asp Arg Leu Arg Val Arg Arg Ser Thr  
215 220 225  
Ala Glu Ala Ala Arg Ile Ile Tyr Pro Pro Glu Ala Gln Thr Ile  
230 235 240  
Ile Val Thr Lys Gly Gln Ser Leu Ile Leu Glu Cys Val Ala Ser  
245 250 255  
Gly Ile Pro Pro Pro Arg Val Thr Trp Ala Lys Asp Gly Ser Ser  
260 265 270

Val Thr Gly Tyr Asn Lys Thr Arg Phe Leu Leu Ser Asn Leu Leu  
 275 280 285  
 Ile Asp Thr Thr Ser Glu Glu Asp Ser Gly Thr Tyr Arg Cys Met  
 290 295 300  
 Ala Asp Asn Gly Val Gly Gln Pro Gly Ala Ala Val Ile Leu Tyr  
 305 310 315  
 Asn Val Gln Val Phe Glu Pro Pro Glu Val Thr Met Glu Leu Ser  
 320 325 330  
 Gln Leu Val Ile Pro Trp Gly Gln Ser Ala Lys Leu Thr Cys Glu  
 335 340 345  
 Val Arg Gly Asn Pro Pro Pro Ser Val Leu Trp Leu Arg Asn Ala  
 350 355 360  
 Val Pro Leu Ile Ser Ser Gln Arg Leu Arg Leu Ser Arg Arg Ala  
 365 370 375  
 Leu Arg Val Leu Ser Met Gly Pro Glu Asp Glu Gly Val Tyr Gln  
 380 385 390  
 Cys Met Ala Glu Asn Glu Val Gly Ser Ala His Ala Val Val Gln  
 395 400 405  
 Leu Arg Thr Ser Arg Pro Ser Ile Thr Pro Arg Leu Trp Gln Asp  
 410 415 420  
 Ala Glu Leu Ala Thr Gly Thr Pro Pro Val Ser Pro Ser Lys Leu  
 425 430 435  
 Gly Asn Pro Glu Gln Met Leu Arg Gly Gln Pro Ala Leu Pro Arg  
 440 445 450  
 Pro Pro Thr Ser Val Gly Pro Ala Ser Pro Lys Cys Pro Gly Glu  
 455 460 465  
 Lys Gly Gln Gly Ala Pro Ala Glu Ala Pro Ile Ile Leu Ser Ser  
 470 475 480  
 Pro Arg Thr Ser Lys Thr Asp Ser Tyr Glu Leu Val Trp Arg Pro  
 485 490 495  
 Arg His Glu Gly Ser Gly Arg Ala Pro Ile Leu Tyr Tyr Val Val  
 500 505 510  
 Lys His Arg Lys Gln Val Thr Asn Ser Ser Asp Asp Trp Thr Ile  
 515 520 525  
 Ser Gly Ile Pro Ala Asn Gln His Arg Leu Thr Leu Thr Arg Leu  
 530 535 540  
 Asp Pro Gly Ser Leu Tyr Glu Val Glu Met Ala Ala Tyr Asn Cys  
 545 550 555  
 Ala Gly Glu Gly Gln Thr Ala Met Val Thr Phe Arg Thr Gly Arg

560	565	570
Arg Pro Lys Pro Glu Ile Met Ala Ser	Lys Glu Gln Gln Ile Gln	
575	580	585
Arg Asp Asp Pro Gly Ala Ser Pro Gln	Ser Ser Ser Gln Pro Asp	
590	595	600
His Gly Arg Leu Ser Pro Pro Glu Ala	Pro Asp Arg Pro Thr Ile	
605	610	615
Ser Thr Ala Ser Glu Thr Ser Val Tyr	Val Thr Trp Ile Pro Arg	
620	625	630
Gly Asn Gly Gly Phe Pro Ile Gln Ser	Phe Arg Val Glu Tyr Lys	
635	640	645
Lys Leu Lys Lys Val Gly Asp Trp Ile	Leu Ala Thr Ser Ala Ile	
650	655	660
Pro Pro Ser Arg Leu Ser Val Glu Ile	Thr Gly Leu Glu Lys Gly	
665	670	675
Thr Ser Tyr Lys Phe Arg Val Arg Ala	Leu Asn Met Leu Gly Glu	
680	685	690
Ser Glu Pro Ser Ala Pro Ser Arg Pro	Tyr Val Val Ser Gly Tyr	
695	700	705
Ser Gly Arg Val Tyr Glu Arg Pro Val	Ala Gly Pro Tyr Ile Thr	
710	715	720
Phe Thr Asp Ala Val Asn Glu Thr Thr	Ile Met Leu Lys Trp Met	
725	730	735
Tyr Ile Pro Ala Ser Asn Asn Asn Thr	Pro Ile His Gly Phe Tyr	
740	745	750
Ile Tyr Tyr Arg Pro Thr Asp Ser Asp	Asn Asp Ser Asp Tyr Lys	
755	760	765
Lys Asp Met Val Glu Gly Asp Lys Tyr	Trp His Ser Ile Ser His	
770	775	780
Leu Gln Pro Glu Thr Ser Tyr Asp Ile	Lys Met Gln Cys Phe Asn	
785	790	795
Glu Gly Gly Glu Ser Glu Phe Ser Asn	Val Met Ile Cys Glu Thr	
800	805	810
Lys Ala Arg Lys Ser Ser Gly Gln Pro	Gly Arg Leu Pro Pro Pro	
815	820	825
Thr Leu Ala Pro Pro Gln Pro Pro Leu	Pro Glu Thr Ile Glu Arg	
830	835	840
Pro Val Gly Thr Gly Ala Met Val Ala	Arg Ser Ser Asp Leu Pro	
845	850	855

Tyr Leu Ile Val Gly Val Val Leu Gly Ser Ile Val Leu Ile Ile  
 860 865 870  
 Val Thr Phe Ile Pro Phe Cys Leu Trp Arg Ala Trp Ser Lys Gln  
 875 880 885  
 Lys His Thr Thr Asp Leu Gly Phe Pro Arg Ser Ala Leu Pro Pro  
 890 895 900  
 Ser Cys Pro Tyr Thr Met Val Pro Leu Gly Gly Leu Pro Gly His  
 905 910 915  
 Gln Ala Ser Gly Gln Pro Tyr Leu Ser Gly Ile Ser Gly Arg Ala  
 920 925 930  
 Cys Ala Asn Gly Ile His Met Asn Arg Gly Cys Pro Ser Ala Ala  
 935 940 945  
 Val Gly Tyr Pro Gly Met Lys Pro Gln Gln His Cys Pro Gly Glu  
 950 955 960  
 Leu Gln Gln Gln Ser Asp Thr Ser Ser Leu Leu Arg Gln Thr His  
 965 970 975  
 Leu Gly Asn Gly Tyr Asp Pro Gln Ser His Gln Ile Thr Arg Gly  
 980 985 990  
 Pro Lys Ser Ser Pro Asp Glu Gly Ser Phe Leu Tyr Thr Leu Pro  
 995 1000 1005  
 Asp Asp Ser Thr His Gln Leu Leu Gln Pro His His Asp Cys Cys  
 1010 1015 1020  
 Gln Arg Gln Glu Gln Pro Ala Ala Val Gly Gln Ser Gly Val Arg  
 1025 1030 1035  
 Arg Ala Pro Asp Ser Pro Val Leu Glu Ala Val Trp Asp Pro Pro  
 1040 1045 1050  
 Phe His Ser Gly Pro Pro Cys Cys Leu Gly Leu Val Pro Val Glu  
 1055 1060 1065  
 Glu Val Asp Ser Pro Asp Ser Cys Gln Val Ser Gly Gly Asp Trp  
 1070 1075 1080  
 Cys Pro Gln His Pro Val Gly Ala Tyr Val Gly Gln Glu Pro Gly  
 1085 1090 1095  
 Met Gln Leu Ser Pro Gly Pro Leu Val Arg Val Ser Phe Glu Thr  
 1100 1105 1110  
 Pro Pro Leu Thr Ile  
 1115

<210> 59  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 59  
gggaaacaca gcagtcattg cctgc 25

<210> 60  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 60  
gcacacgttag cctgtcgctg gaga 24

<210> 61  
<211> 42  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-42  
<223> Synthetic construct.

<400> 61  
caccccaaag cccaggtccg gtacagcgtc aaacaagagt gg 42

<210> 62  
<211> 1661  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 678  
<223> unknown base

<400> 62  
cggaggctg ggtcgcatg atccggaccc cattgtcgcc ctctgccc 50  
cgccctgctcc tcccaggctc ccgcggccga cccccgcgca acatgcagcc 100  
cacggggccgc gagggttccc ggcgcgtca ag ccggcggtat ctgcggcg 150  
tgctgctcct gctactgctg ctgctgctgc ggcagccgt aaccgcgcg 200  
gagaccacgc cggcgcccc cagagccctc tccacgctgg gctccccag 250  
cctcttacc accgcgggtg tccccagcgc cctcaactacc ccaggcctca 300  
ctacgccagg caccccaaa accctggacc ttccgggtcg cgccaggcc 350

ctgatgcgga gtttccact cgtggacggc cacaatgacc tgccccaggt 400  
cctgagacag cgttacaaga atgtgcttca ggatgttaac ctgcgaaatt 450  
tcagccatgg tcagaccaggc ctggacaggc ttagagacgg cctcggtgg 500  
gcccgaggctt ggtcagcctc cgtctcatgc cagtcccagg accagactgc 550  
cgtgcgcctc gccctggagc agattgacct cattcaccgc atgtgtgcct 600  
ccctactctga actcgagctt gtgaccttag ctgaaggctt gaacagctct 650  
caaaaagctgg cctgcctcat tggcgtgnag ggtggtaact cactggacag 700  
cagcctctct gtgctgcgca gtttctatgt gctgggggtg cgctacctga 750  
cacttacctt cacctgcagt acaccatggg cagagagttc caccaagttc 800  
agacaccaca tgtacaccaa cgtcagcggg ttgacaagct ttggtgagaa 850  
agtagtagag gagttgaacc gcctgggcat gatgatagat ttgtcctatg 900  
catcggacac cttgataaga agggtcctgg aagtgtctca ggctcctgtg 950  
atcttctccc actcagctgc cagagctgtg tgtgacaatt tggtaatgt 1000  
tccccatgat atcctgcagc ttctgaagaa cgggtggcatc gtgatggta 1050  
cactgtccat gggggtgctg cagtgcacc tgcttgctaa cgtgtccact 1100  
gtggcagatc actttgacca catcaggcgtc gtcattggat ctgagttcat 1150  
cgggatttgtt gaaaaattatg acgggactgg ccgggtccct caggggctgg 1200  
aggatgtgtc cacataacca gtcctgatag aggagttgct gagtcgtasc 1250  
tggagcggagg aagagcttca aggtgtcctt cgtggaaacc tgctgcgggt 1300  
cttcagacaa gtggaaaagg tgagagagga gagcaggcgc cagagcccc 1350  
tggaggctga gtttccatat gggcaactga gcacatcctg ccactccac 1400  
ctcgtgcctc agaatggaca ccaggctact catctggagg tgaccaagca 1450  
gccaaccaat cgggtccct ggaggtcctc aaatgcctcc ccataccttg 1500  
ttccaggcct tgtggctgct gccaccatcc caaccttcac ccagtggctc 1550  
tgctgacaca gtcgggtcccc gcagaggtca ctgtggcaaa gcctcacaaa 1600  
gccccctctc ctagttcatt cacaagcata tgctgagaat aaacatgtta 1650  
cacatggaaa a 1661

<210> 63  
<211> 487  
<212> PRT  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 196, 386  
<223> unknown amino acid

<400> 63

Met	Gln	Pro	Thr	Gly	Arg	Glu	Gly	Ser	Arg	Ala	Leu	Ser	Arg	Arg
1				5				10					15	
Tyr	Leu	Arg	Arg	Leu	Arg									
				20				25					30	
Gln	Pro	Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala
				35				40					45	
Leu	Ser	Thr	Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val
				50				55					60	
Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro
				65				70					75	
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser
				80				85					90	
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg
				95				100					105	
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe
				110				115					120	
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val
				125				130					135	
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp
				140				145					150	
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His
				155				160					165	
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala
				170				175					180	
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val
				185				190					195	
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser
				200				205					210	
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys
				215				220					225	
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met
				230				235					240	
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val
				245				250					255	
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala

260	265	270
Ser Asp Thr Leu Ile Arg Arg Val Leu Glu Val Ser Gln Ala Pro		
275	280	285
Val Ile Phe Ser His Ser Ala Ala Arg Ala Val Cys Asp Asn Leu		
290	295	300
Leu Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Asn Gly Gly		
305	310	315
Ile Val Met Val Thr Leu Ser Met Gly Val Leu Gln Cys Asn Leu		
320	325	330
Leu Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Arg		
335	340	345
Ala Val Ile Gly Ser Glu Phe Ile Gly Ile Gly Gly Asn Tyr Asp		
350	355	360
Gly Thr Gly Arg Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr		
365	370	375
Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Xaa Trp Ser Glu Glu		
380	385	390
Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg		
395	400	405
Gln Val Glu Lys Val Arg Glu Glu Ser Arg Ala Gln Ser Pro Val		
410	415	420
Glu Ala Glu Phe Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser		
425	430	435
His Leu Val Pro Gln Asn Gly His Gln Ala Thr His Leu Glu Val		
440	445	450
Thr Lys Gln Pro Thr Asn Arg Val Pro Trp Arg Ser Ser Asn Ala		
455	460	465
Ser Pro Tyr Leu Val Pro Gly Leu Val Ala Ala Ala Thr Ile Pro		
470	475	480
Thr Phe Thr Gln Trp Leu Cys		
485		

<210> 64  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 64

ccttcacccg cagtacacca tgggc 25

<210> 65  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 65  
gtcacacacaca gctctggcag ctgag 25

<210> 66  
<211> 47  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-47  
<223> Synthetic construct.

<400> 66  
ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaaggc 47

<210> 67  
<211> 1564  
<212> DNA  
<213> Homo sapiens

<400> 67  
tgctaggctc tgtcccacaa tgcacccgag agcaggagct gaaaggcctct 50  
aacacccaca gatccctcta tgactgaat gtgaggtgtc cggctttgct 100  
ggcccagcaa gcctgataag catgaagctc ttatcttgg tggctgtgtt 150  
cgggtgttttgc ctgggtcccc cagctgaagc caacaagagt tctgaagata 200  
tccggtgcaa atgcacatgt ccaccttata gaaacatcag tggcacatt 250  
tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtgggtgga 300  
gcccatgcca gtgcctggcc atgacgtgga ggcctactgc ctgctgtgcg 350  
agtgcaggta cgaggagcgc agcaccacca ccatcaaggt catcattgtc 400  
atctacatgt ccgtgggtgg tgcctgttg ctctacatgg ctttcctgtat 450  
gctgggtggac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500  
acaatgagga ggagaatgag gatgctcgct ctatggcagc agctgctgca 550  
tccctcgaaaa gaccccgagc aaacacagtc ctggagcgtg tggaaagggtgc 600

ccagcagcgg tggaaagctgc aggtgcagga gcagcggaaag acagtcttcg 650  
atccggcacaa gatgctcagc tagatgggct ggtgtggttt ggtcaaggcc 700  
ccaaacaccat ggctgccagc ttccaggctg gacaaagcag ggggctactt 750  
ctcccttccc tcgggttccag tcttccctt aaaagcctgt ggcattttc 800  
ctccttctcc ctaactttag aaatgttcta cttggctatt ttgatttaggg 850  
aagagggatg tggtctctga tctctgttgt cttcttggtt ctgggggtt 900  
gaagggaggg ggaaggcagg ccagaaggga atggagacat tcgagggggc 950  
ctcaggagtg gatgcgatct gtctctcctg gctccactct tgccgccttc 1000  
cagctctgag tcttggaaat gttgttaccc ttggaagata aagctgggtc 1050  
ttcaggaact cagtgtctgg gagaaagca tggcccagca ttcagcatgt 1100  
gttcctttct gcagtggttc ttatcaccac ctccctccca gccccggcgc 1150  
ctcagccccca gccccagctc cagccctgag gacagctctg atgggagagc 1200  
tgggccccct gagcccactg ggtcttcagg gtgcactgga agctgggtt 1250  
cgctgtcccc tttgtcacttc tcgcactggg gcatggagtg cccatgcata 1300  
ctctgctgcc ggtccccctca cctgcacttg aggggtctgg gcagtcctc 1350  
ctctccccag tgtccacagt cactgagcca gacggtcggg tggaaacatga 1400  
gactcgaggc ttagcgtgga tctgaacacc acagccccctg tactgggtt 1450  
gcctcttgcc cctgaacttc gttgtaccag tgcattggaga gaaaattttg 1500  
tctcttgcc tttaggttgt gtgtaaatca aggaagccat cattaaattt 1550  
tttttatttct ctca 1564

<210> 68  
<211> 183  
<212> PRT  
<213> *Homo sapiens*

<400> 68

Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val  
1 5 10 15

Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys  
20 25 30

Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn  
35 40 45

Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu  
50 55 60

Pro Met Pro Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu  
                   65                  70                  75  
 Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val  
                   80                  85                  90  
 Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu Leu Leu Tyr  
                   95                  100                105  
 Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys Pro Asp  
                   110                115                120  
 Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp Ala  
                   125                130                135  
 Arg Ser Met Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala  
                   140                145                150  
 Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys  
                   155                160                165  
 Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys  
                   170                175                180  
 Met Leu Ser

<210> 69  
 <211> 3170  
 <212> DNA  
 <213> Homo sapiens

<400> 69  
 agcgggtctc gcttgggttc cgctaatttc tgcctgagg cgtgagactg 50  
 agttcatagg gtcctgggtc cccgaaccag gaagggttga gggAACACAA 100  
 tctgcaagcc cccgcacccc aagtggggg ccccggttg gggcctccc 150  
 tccctttgca ttccccacccc tccgggctt gcgtcttcct ggggACCCCC 200  
 tcggccggag atggccgcgt tgatgcggag caaggattcg tcctgctgcc 250  
 tgctcctact ggccgcgtg ctgatggtgg agagctaca gatcggcagt 300  
 tcgcgggcca aactcaactc catcaagtcc tctctggcgt gggagacgcc 350  
 tggtcaggcc gccaatcgat ctgcgggcat gtaccaagga ctggcattcg 400  
 gccgcgtaa gaaggcAAA aacctggggc aggctaccc ttgttagcagt 450  
 gataaggagt gtgaagttgg gaggtattgc cacagtcccc accaaggatc 500  
 atcggcctgc atggtgtgtc ggagaaaaaa gaagcgctgc caccgagatg 550  
 gcatgtgctg ccccagtacc cgctgcaata atggcatctg tatcccagtt 600  
 actgaaagca tcttaacccc tcacatcccg gctctggatg gtactcggca 650

cagagatcga aaccacggtc attactcaaa ccatgacttg ggatggcaga 700  
atcttaggaag accacacact aagatgtcac atataaaagg gcatgaagga 750  
gaccctgcc tacgatcatc agactgcatt gaagggtttt gctgtgctcg 800  
tcatttctgg accaaaatct gcaaaccagt gctccatcaig gggaaagtct 850  
gtaccaaaca acgcaagaag gttctcatg ggctggaaat tttccagcgt 900  
tgcgactgtg cgaagggcct gtcttgcaaa gtatggaaag atgccaccta 950  
ctcctccaaa gccagactcc atgtgtgtca gaaaatttga tcaccattga 1000  
ggaacatcat caattgcaga ctgtgaagtt gtgtattta tgcattatag 1050  
catggtgaa aataaggttc agatgcagaa gaatggctaa aataagaaac 1100  
gtgataagaa tatagatgtat cacaaaaagg gagaaagaaa acatgaactg 1150  
aatagattag aatgggtgac aaatgcagtg cagccagtgt ttccattatg 1200  
caacttgtct atgtaaataa tgtacacatt tgtggaaaat gctattatta 1250  
agagaacaag cacacagtgg aaattactga tgagtagcat gtgactttcc 1300  
aagagtttag gttgtgctgg aggagaggtt tccttcagat tgctgattgc 1350  
ttatacaaataat aacctacatg ccagatttctt attcaacgtt agagtttaac 1400  
aaaatactcc tagaataact tgttatacaa taggttctaa aaataaaatt 1450  
gctaaacaag aaatgaaaac atggagcatt gttatattac aacagaaaat 1500  
taccttttga tttgtAACAC tacttctgtt gttcaatcaa gagttttgtt 1550  
agataagaaa aaaatcagtc aatatttcca aataattgca aaataatggc 1600  
cagttgttta ggaaggcctt taggaagaca aataaataac aaacaaacag 1650  
ccacaaatac tttttttca aaatttttagt ttacacctgtt attaataaga 1700  
actgatacaa gacaaaaaca gttccttcag attctacggta atgacagtat 1750  
atctctctttt atcctatgtt atccctgctc tgaatgcatt atattttcca 1800  
aactataccca ataaattgtt actagtaaaa tacttacaca gagcagaatt 1850  
ttcacagatg gcaaaaaaaat ttaaaagatgt ccaatatatg tggaaaaga 1900  
gctaacagag agatcattat ttcttaaaga ttggccataa cctatatttt 1950  
gatagaatta gattggtaaa tacatgtatt catacatact ctgtggtaat 2000  
agagacttaa gctggatctg tactgcactg gagtaagcaa gaaaattggg 2050  
aaaactttttt cgtttggtaa ggtttggca acacatagat catatgtctg 2100

aggcacaagt tggctgttca tctttgaaac cagggatgc acagtctaaa 2150  
tgaatatctg catggattt gctatcataa tatttactat gcagataat 2200  
tcagtgttag gtcctgtgtc cgtactatcc tcaaattatt tattttatag 2250  
tgctgagatc ctcaaataat ctcaatttca ggaggttca caaaatgtac 2300  
tcctgaagta gacagagtag tgaggttca ttgcctcta taagcttctg 2350  
actagccaat ggcatcatcc aattttcttc ccaaacctct gcagcatctg 2400  
ctttattgcc aaagggttag ttccgggtt ctgcagccat tgccgttaaa 2450  
aaatataagt aggataactt gtaaaacctg catattgcta atctatagac 2500  
accacagttt ctaaattctt tgaaaccact ttactacttt ttttaaactt 2550  
aactcagttc taaatacttt gtctggagca caaaacaata aaaggttac 2600  
ttatagtcgt gactttaaac tttttagac cacaattcac ttttagttt 2650  
tctttactt aaatcccattc tgcaatctca aatttaagtt ctcccagtag 2700  
agattgagtt tgagcctgta tatctattaa aaatttcaac ttcccacata 2750  
tatctactaa gatgattaag acttacattt tctgcacagg tctgcacaaaa 2800  
caaaaattat aaactagtcc atccaagaac caaagttgt ataaacaggt 2850  
tgctataagc ttgtgaaatg aaaatgaaac atttcaatca aacatttcct 2900  
atataacaat tattatattt acaatttggt ttctgcaata ttttcttat 2950  
gtccaccctt ttaaaaatta ttatttgaag taatttattt acaggaaatg 3000  
ttaatgagat gtattttctt atagagatat ttcttacaga aagctttgta 3050  
gcagaatata tttgcagcta ttgactttgt aatttagaa aatgtataa 3100  
taagataaaaa tctattaaat ttttctcctc taaaaactga aaaaaaaaaa 3150  
aaaaaaaaaaaa aaaaaaaaaa 3170

<210> 70  
<211> 259  
<212> PRT  
<213> Homo sapiens

<400> 70  
Met Ala Ala Leu Met Arg Ser Lys Asp Ser Ser Cys Cys Leu Leu  
1 5 10 15  
Leu Leu Ala Ala Val Leu Met Val Glu Ser Ser Gln Ile Gly Ser  
20 25 30  
Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly Glu  
35 40 45

Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly  
 50 55 60  
 Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala  
 65 70 75  
 Tyr Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys  
 80 85 90  
 His Ser Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg  
 95 100 105  
 Lys Lys Lys Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr  
 110 115 120  
 Arg Cys Asn Asn Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu  
 125 130 135  
 Thr Pro His Ile Pro Ala Leu Asp Gly Thr Arg His Arg Asp Arg  
 140 145 150  
 Asn His Gly His Tyr Ser Asn His Asp Leu Gly Trp Gln Asn Leu  
 155 160 165  
 Gly Arg Pro His Thr Lys Met Ser His Ile Lys Gly His Glu Gly  
 170 175 180  
 Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly Phe Cys Cys  
 185 190 195  
 Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu His Gln  
 200 205 210  
 Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly Leu  
 215 220 225  
 Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys  
 230 235 240  
 Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val  
 245 250 255  
 Cys Gln Lys Ile

<210> 71  
 <211> 1809  
 <212> DNA  
 <213> Homo sapiens

<400> 71  
 tctcaatctg ctgacacctcgatccgcctg accttgtaat ccacctac 50  
 tggcctccca aagtgttggg attacaggcg tgagccaccg cgccccggcca 100  
 acatcacgtt tttaaaaatt gatttcttca aattcatggc aaatatttcc 150  
 cttcccttta acttcttatg tcagaatgag gaaggatagc tgcatttatt 200

tagtcagttt tcattgcata gtaatatttt catgtatcat tttctaagtt 250  
atattttagt aattcatatg ttttagatta taggtttaa catacttg 300  
aaaatactg atgtgttta aagccttggg cagaaattct gtattgtga 350  
ggatttgttc ttttatcccc cttaaagt catccgtcct tggctcagga 400  
tttggagagc ttgcaccacc aaaaatggca aacatcacca gctcccagat 450  
tttggaccag ttgaaagctc cgagtttggg ccagtttacc accaccccaa 500  
gtacacagca gaatagtaca agtcacccca caactactac ttcttggac 550  
ctcaagcccc caacatccca gtcctcagtc ctcagtcattc ttgacttcaa 600  
atctcaacct gagccatccc cagttcttag ccagttgagc cagcgacaac 650  
agcaccagag ccaggcagtc actgttcctc ctccctggg ggagtcctt 700  
ccttcccagg caaaacttcg agaatcaaca cctggagaca gtccctccac 750  
tgtgaacaag ctttgcagc ttcccagcac gaccattgaa aatatctctg 800  
tgtctgtcca ccagccacag cccaaacaca tcaaacttgc taagcggcgg 850  
ataccccccag cttctaagat cccagttct gcagtgaaa tgcctggg 900  
agcagatgtc acaggattaa atgtgcagtt tggttgcattg gaatttgggt 950  
cagaacccctc tctctgaa ttggatcag ctccaagcag tgaaaatagt 1000  
aatcagattc ccatcagctt gtattcgaag tcttaagtg agccttggaa 1050  
tacatcttta tcaatgacca gtgcagtaca gaactccaca tataacaactt 1100  
ccgtcattac ctcctgcagt ctgacaagct catcaactgaa ttctgctagt 1150  
ccagtagcaa tgtcttcctc ttatgaccag agttctgtgc ataacaggat 1200  
cccataccaa agccctgtga gttcatcaga gtcagctcca ggaaccatca 1250  
tgaatggaca tggtggtggt cgaagtcagc agacactaga cagtaagtat 1300  
agcagcaagc tactcttgc atggctgggt ccaaccaaac agaggaagag 1350  
gatagctcac gtgatgtgga aaacaccagt tggtaatgg ctcattcggt 1400  
aaaaagcagc cctttgctt tttgtttt ggaccagggtg ttggctgtgg 1450  
tgttattaga aatgtcttaa ccacagcaag aaggagggtgg tggctcata 1500  
ttcttctgcc ctaatcagac tgcaccacaa gtgcagcata cagttatgt 1550  
tttaaagatg cttggccag gcgggggtggc tggatgccc aatcccagtg 1600  
ctttgggggg ccaaggcagg cagattgccca aagctcagga gtttgagacc 1650

accctggca acatggtaa actctgtctc tactaaaata cgaaaaacta 1700  
 gccgggtgtg gtggcgccgc gtgcctgtaa tcccagctac ttgggaggct 1750  
 gaggcacaag aatcgcttga gccagcttgg gctacaaagt gagactccgt 1800  
 ctgaaaaga 1809

<210> 72  
 <211> 363  
 <212> PRT  
 <213> Homo sapiens

<400> 72  
 Met Cys Phe Lys Ala Leu Gly Arg Asn Ser Val Leu Leu Arg Ile  
 1 5 10 15

Cys	Ser	Phe	Ile	Pro	Leu	Leu	Lys	Ser	Ser	Val	Leu	Gly	Ser	Gly
				20				25						30

Phe	Gly	Glu	Leu	Ala	Pro	Pro	Lys	Met	Ala	Asn	Ile	Thr	Ser	Ser
				35				40						45

Gln	Ile	Leu	Asp	Gln	Leu	Lys	Ala	Pro	Ser	Leu	Gly	Gln	Phe	Thr
				50				55						60

Thr	Thr	Pro	Ser	Thr	Gln	Gln	Asn	Ser	Thr	Ser	His	Pro	Thr	Thr
				65				70						75

Thr	Thr	Ser	Trp	Asp	Leu	Lys	Pro	Pro	Thr	Ser	Gln	Ser	Ser	Val
				80				85						90

Leu	Ser	His	Leu	Asp	Phe	Lys	Ser	Gln	Pro	Glu	Pro	Ser	Pro	Val
				95				100						105

Leu	Ser	Gln	Leu	Ser	Gln	Arg	Gln	Gln	His	Gln	Ser	Gln	Ala	Val
				110				115						120

Thr	Val	Pro	Pro	Pro	Gly	Leu	Glu	Ser	Phe	Pro	Ser	Gln	Ala	Lys
				125				130						135

Leu	Arg	Glu	Ser	Thr	Pro	Gly	Asp	Ser	Pro	Ser	Thr	Val	Asn	Lys
				140				145						150

Leu	Leu	Gln	Leu	Pro	Ser	Thr	Thr	Ile	Glu	Asn	Ile	Ser	Val	Ser
				155				160						165

Val	His	Gln	Pro	Gln	Pro	Lys	His	Ile	Lys	Leu	Ala	Lys	Arg	Arg
				170				175						180

Ile	Pro	Pro	Ala	Ser	Lys	Ile	Pro	Ala	Ser	Ala	Val	Glu	Met	Pro
				185				190						195

Gly	Ser	Ala	Asp	Val	Thr	Gly	Leu	Asn	Val	Gln	Phe	Gly	Ala	Leu
				200				205						210

Glu	Phe	Gly	Ser	Glu	Pro	Ser	Leu	Ser	Glu	Phe	Gly	Ser	Ala	Pro
				215				220						225

Ser Ser Glu Asn Ser Asn Gln Ile Pro Ile Ser Leu Tyr Ser Lys  
230 235 240

Ser Leu Ser Glu Pro Leu Asn Thr Ser Leu Ser Met Thr Ser Ala  
245 250 255

Val Gln Asn Ser Thr Tyr Thr Thr Ser Val Ile Thr Ser Cys Ser  
260 265 270

Leu Thr Ser Ser Leu Asn Ser Ala Ser Pro Val Ala Met Ser  
275 280 285

Ser Ser Tyr Asp Gln Ser Ser Val His Asn Arg Ile Pro Tyr Gln  
290 295 300

Ser Pro Val Ser Ser Ser Glu Ser Ala Pro Gly Thr Ile Met Asn  
305 310 315

Gly His Gly Gly Arg Ser Gln Gln Thr Leu Asp Ser Lys Tyr  
320 325 330

Ser Ser Lys Leu Leu Ser Trp Leu Val Pro Thr Lys Gln Arg  
335 340 345

Lys Arg Ile Ala His Val Met Trp Lys Thr Pro Val Gly Gln Trp  
350 355 360

Leu Ile Arg

<210> 73  
<211> 26  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-26  
<223> Synthetic construct.

<400> 73  
aattcatggc aaatatttcc cttccc 26

<210> 74  
<211> 22  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-22  
<223> Synthetic construct.

<400> 74  
tggtaaactg gcccaaactc gg 22

<210> 75  
<211> 50

<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-50  
<223> Synthetic construct

<400> 75  
ttaaagtcat ccgtccttgg ctcaggattt ggagagcttg caccaccaaa 50

<210> 76  
<211> 1989  
<212> DNA  
<213> Homo sapiens

<400> 76  
gccgagtgcc acaaagcctg gggctggcg gggccatgg cgctgccatc 50  
ccgaatcctg ctttggaaac ttgtgcttct gcagagctct gctgttctcc 100  
tgcactcagc ggtggaggag acggacgcgg ggctgtacac ctgcaacctg 150  
caccatcact actgccaccc ttagagagc ctggccgtcc gcctggaggt 200  
caccgacggc ccccccggcca ccccccgccta ctgggacggc gagaaggagg 250  
tgctggcggt ggcgcgcggc gcacccgcgc ttctgacctg cgtgaaccgc 300  
gggcacgtgt ggaccgaccg gcacgtggag gaggctcaac aggtggtgca 350  
ctgggaccgg cagccgcgg gggtcccgca cgaccgcgcg gaccgcctgc 400  
tggacctcta cgcgtcggc gagcgccgcg cctacgggcc ccttttctg 450  
cgcgaccgcg tggctgtgg cgccgatgcc tttgagcgcg gtgacttctc 500  
actgcgtatc gagccgctgg aggtcgccga cgagggcacc tactcctgcc 550  
acctgcacca ccattactgt ggcctgcacg aacgcgcgt cttccacctg 600  
acggtcgccc aaccccacgc ggagccgccc ccccgccccct ctccgggcaa 650  
cggtccagg cacagcggcg ccccaaggccc agacccaca ctggcgcgcg 700  
gccacaacgt catcaatgtc atcgccccg agagccgagc ccacttctc 750  
cagcagctgg gctacgtgct ggccacgctg ctgctttca tcctgctact 800  
ggtcactgtc ctccctggccg cccgcaggcg ccgcggaggc tacgaataact 850  
cggaccagaa gtcggaaag tcaaaggaga aggatgttaa ctggcggag 900  
ttcgctgtgg ctgcaggaga ccagatgctt tacaggagtg aggacatcca 950  
gctagattac aaaaacaaca tcctgaagga gagggcggag ctggcccaca 1000  
gccccctgcc tgccaagtac atcgacctag acaaagggtt ccggaaaggag 1050

aactgcaaat agggaggccc tgggctcctg gctgggccag cagctgcacc 1100  
tctcctgtct gtgctcctcg ggcatctcc tcatgctccg gggctcaccc 1150  
cccttccagc ggctggtccc gcttcctgg aatttggcct gggcgtatgc 1200  
agaggccgccc tccacacccc tcccccaggg gcttggtggc agcatagccc 1250  
ccacccctgc ggccttgct cacgggtggc cctgcccacc cctggcacaa 1300  
ccaaaatccc actgatgccc atcatgccc cagacccttc tgggctctgc 1350  
ccgctggggg cctgaagaca ttccctggagg acactccat cagaacctgg 1400  
cagccccaaa actggggtca gcctcagggc aggagtccca ctccctccagg 1450  
gctctgctcg tccggggctg ggagatgttc ctggaggagg acactccat 1500  
cagaacttgg cagccttgaa gttggggtca gcctcggcag gagtcccact 1550  
cctcctgggg tgctgcctgc caccaagagc tcccccacct gtaccaccat 1600  
gtgggactcc aggcaccatc ttttctcccc agggacctgc tgacttgaat 1650  
gccagccctt gtcctctgt gttgcttgg gccacctgg gctgcacccc 1700  
ctgcccctttc tctgccccat ccctacccta gccttgctct cagccaccc 1750  
gatagtcact gggctccctg tgacttctga ccctgacacc cctcccttgg 1800  
actctgcctg ggctggagtc tagggctggg gctacatttgc ttctgtac 1850  
tggctgagga caggggaggg agtgaagttg gtttggggtg gcctgtgttg 1900  
ccactctcag caccccacat ttgcatctgc tggtgacact gccaccatca 1950  
caataaagtc cccatctgat tttaaaaaaaaaaaaaaa 1989

<210> 77  
<211> 341  
<212> PRT  
<213> Homo sapiens

<400> 77  
Met Ala Leu Pro Ser Arg Ile Leu Leu Trp Lys Leu Val Leu Leu  
1 5 10 15  
Gln Ser Ser Ala Val Leu Leu His Ser Ala Val Glu Glu Thr Asp  
20 25 30  
Ala Gly Leu Tyr Thr Cys Asn Leu His His His Tyr Cys His Leu  
35 40 45  
Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro Pro  
50 55 60  
Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val  
65 70 75

Ala	Arg	Gly	Ala	Pro	Ala	Leu	Leu	Thr	Cys	Val	Asn	Arg	Gly	His
80									85					90
Val	Trp	Thr	Asp	Arg	His	Val	Glu	Glu	Ala	Gln	Gln	Val	Val	His
95									100					105
Trp	Asp	Arg	Gln	Pro	Pro	Gly	Val	Pro	His	Asp	Arg	Ala	Asp	Arg
110									115					120
Leu	Leu	Asp	Leu	Tyr	Ala	Ser	Gly	Glu	Arg	Arg	Ala	Tyr	Gly	Pro
125									130					135
Leu	Phe	Leu	Arg	Asp	Arg	Val	Ala	Val	Gly	Ala	Asp	Ala	Phe	Glu
140									145					150
Arg	Gly	Asp	Phe	Ser	Leu	Arg	Ile	Glu	Pro	Leu	Glu	Val	Ala	Asp
155									160					165
Glu	Gly	Thr	Tyr	Ser	Cys	His	Leu	His	His	His	Tyr	Cys	Gly	Leu
170									175					180
His	Glu	Arg	Arg	Val	Phe	His	Leu	Thr	Val	Ala	Glu	Pro	His	Ala
185									190					195
Glu	Pro	Pro	Pro	Arg	Gly	Ser	Pro	Gly	Asn	Gly	Ser	Ser	His	Ser
200									205					210
Gly	Ala	Pro	Gly	Pro	Asp	Pro	Thr	Leu	Ala	Arg	Gly	His	Asn	Val
215									220					225
Ile	Asn	Val	Ile	Val	Pro	Glu	Ser	Arg	Ala	His	Phe	Phe	Gln	Gln
230									235					240
Leu	Gly	Tyr	Val	Leu	Ala	Thr	Leu	Leu	Phe	Ile	Leu	Leu	Leu	
245									250					255
Val	Thr	Val	Leu	Leu	Ala	Ala	Arg	Arg	Arg	Gly	Gly	Tyr	Glu	
260									265					270
Tyr	Ser	Asp	Gln	Lys	Ser	Gly	Lys	Ser	Lys	Gly	Lys	Asp	Val	Asn
275									280					285
Leu	Ala	Glu	Phe	Ala	Val	Ala	Ala	Gly	Asp	Gln	Met	Leu	Tyr	Arg
290									295					300
Ser	Glu	Asp	Ile	Gln	Leu	Asp	Tyr	Lys	Asn	Asn	Ile	Leu	Lys	Glu
305									310					315
Arg	Ala	Glu	Leu	Ala	His	Ser	Pro	Leu	Pro	Ala	Lys	Tyr	Ile	Asp
320									325					330
Leu	Asp	Lys	Gly	Phe	Arg	Lys	Glu	Asn	Cys	Lys				
335									340					

<210> 78

<211> 2243

<212> DNA

<213> Homo sapiens

<400> 78

cgccggaggc agcggcggcg tggcgcagcg gcgacatggc cgttgtctca 50  
gaggacgact ttcatcacag ttcaaactcc acctacggaa ccacaaggcag 100  
cagtctccga gctgaccagg aggcaactgct tgagaagctg ctggaccgcc 150  
cgccccctgg cctgcagagg cccgaggacc gcttctgtgg cacatacatc 200  
atcttcttca gcctgggcat tggcagtcta ctgccatggc acttctttat 250  
cactgccaag gagtaactgga tgttcaaact cccgcaactcc tccagcccag 300  
ccaccgggga ggacccttag ggctcagaca tcctgaacta ctttgagagc 350  
taccttgcgg ttcctccac cgtgcctcc atgctgtgcc tggtgccaa 400  
cttcctgctt gtcaacaggg ttgcagtcca catccgtgtc ctggcctcac 450  
tgacggtcat cctggccatc ttcatggtga taactgcact ggtgaaggtg 500  
gacacttcctt cctggaccgg tggttttttt gcggtcacca ttgtctgcat 550  
ggtgatcctc agcggtgcct ccactgtctt cagcagcagc atctacggca 600  
tgaccggctc ctttcctatg aggaactccc aagcaactgat atcaggagga 650  
gccatgggcg ggacggtcag cgccgtggcc tcattggtgg acttggctgc 700  
atccagtatgt gtgaggaaca gcgccctggc ctttcctctg acggccacca 750  
tcttcctcggt gctctgcattt ggactctacc tgctgtgtc caggctggag 800  
tatgccaggt actacatgag gcctgttctt gcggcccatg tggggctgg 850  
tgaagaggag cttccccagg actccctcag tgcccttcg gtggcctcca 900  
gattcattga ttccccacaca cccctctcc gccccatcct gaagaagacg 950  
gccagcctgg gcttctgtgt cacctacgtc ttcttcatca ccagcctcat 1000  
ctaccccgcc gtctgcacca acatcgagtc cctcaacaag ggctcgggct 1050  
cactgtggac caccaagttt ttcatcccccc tcactacctt cttctgtac 1100  
aactttgctg acctatgtgg cccgcagctc accgcctggc tccaggtgcc 1150  
agggcccaac agcaaggcgc tcccagggtt cgtgcctctc cggacctgcc 1200  
tcatccccctt cttcgtgtc tgtaactacc agccccgcgt ccacctgaag 1250  
actgtggtct tccagtcga tggtaaccgc gcaactctca gctccctgct 1300  
ggggctcagc aacggctacc tcagcaccctt ggccttcctc tacgggccta 1350  
agattgtgcc cagggagctg gctgaggcca cgggagtggt gatgtccctt 1400  
tatgtgtgct tgggcttaac actgggctca gcctgctcta ccctcctgg 1450

gcacacctatc tagaagggag gacacaagga cattgggtct tcagagcctt 1500  
 tgaagatgag aagagagtgc aggagggctg gggccatgg aggaaaggcc 1550  
 taaagttca cttggggaca gagagcagag cacactcggg cctcatccct 1600  
 cccaagatgc cagttagcca cgtccatgcc cattccgtgc aaggcagata 1650  
 ttccagtcat attaacagaa cactcctgag acagttgaag aagaaatagc 1700  
 acaaattcagg ggtactccct tcacagctga tggtaacat tccaccttct 1750  
 ttctagccct tcaaagatgc tgccagtggtt cgccctagag ttattacaaa 1800  
 gccagtgcctt aaaccctagcc atgggctt tgcaacctcc cagctgcgt 1850  
 cattccagct gacagcgaga tgcaagcaaa tgctcagctc tccttaccct 1900  
 gaaggggtct ccctggaatg gaagtcccctt ggcattgtca gtcctcaggc 1950  
 ccaagactca agtgtgcaca gaccctgtg ttctgcgggt gaacaactgc 2000  
 ccactaaccctt gactggaaaa cccagaaaga tggcccttcc atgaatgctt 2050  
 cattccagag ggaccagagg gcctccctgt gcaagggatc aagcatgtct 2100  
 ggcctgggtt ttcaaaaaaaaaa gagggtcctt catgacctgg tggtctatgg 2150  
 cctgggtcaa gatgagggtc tttcagtggtt cctgtttaca acatgtcaaa 2200  
 gccattgggtt caagggcgta ataaatactt gcgtattcaa aaa 2243

<210> 79

<211> 475

<212> PRT

<213> Homo sapiens

<400> 79

Met	Ala	Val	Val	Ser	Glu	Asp	Asp	Phe	Gln	His	Ser	Ser	Asn	Ser
1														15

Thr	Tyr	Gly	Thr	Thr	Ser	Ser	Ser	Leu	Arg	Ala	Asp	Gln	Glu	Ala
														30

Leu	Leu	Glu	Lys	Leu	Leu	Asp	Arg	Pro	Pro	Gly	Leu	Gln	Arg

Pro	Glu	Asp	Arg	Phe	Cys	Gly	Thr	Tyr	Ile	Ile	Phe	Phe	Ser	Leu

Gly	Ile	Gly	Ser	Leu	Leu	Pro	Trp	Asn	Phe	Phe	Ile	Thr	Ala	Lys

Glu	Tyr	Trp	Met	Phe	Lys	Leu	Arg	Asn	Ser	Ser	Ser	Pro	Ala	Thr

Gly	Glu	Asp	Pro	Glu	Gly	Ser	Asp	Ile	Leu	Asn	Tyr	Phe	Glu	Ser

Tyr Leu Ala Val Ala Ser Thr Val Pro Ser Met Leu Cys Leu Val  
 110 115 120  
 Ala Asn Phe Leu Leu Val Asn Arg Val Ala Val His Ile Arg Val  
 125 130 135  
 Leu Ala Ser Leu Thr Val Ile Leu Ala Ile Phe Met Val Ile Thr  
 140 145 150  
 Ala Leu Val Lys Val Asp Thr Ser Ser Trp Thr Arg Gly Phe Phe  
 155 160 165  
 Ala Val Thr Ile Val Cys Met Val Ile Leu Ser Gly Ala Ser Thr  
 170 175 180  
 Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser Phe Pro Met  
 185 190 195  
 Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly Gly Thr  
 200 205 210  
 Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser Asp  
 215 220 225  
 Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Ile Phe  
 230 235 240  
 Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu  
 245 250 255  
 Tyr Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe  
 260 265 270  
 Ser Gly Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser  
 275 280 285  
 Val Ala Ser Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro  
 290 295 300  
 Ile Leu Lys Lys Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val  
 305 310 315  
 Phe Phe Ile Thr Ser Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile  
 320 325 330  
 Glu Ser Leu Asn Lys Gly Ser Gly Ser Leu Trp Thr Thr Lys Phe  
 335 340 345  
 Phe Ile Pro Leu Thr Thr Phe Leu Leu Tyr Asn Phe Ala Asp Leu  
 350 355 360  
 Cys Gly Arg Gln Leu Thr Ala Trp Ile Gln Val Pro Gly Pro Asn  
 365 370 375  
 Ser Lys Ala Leu Pro Gly Phe Val Leu Leu Arg Thr Cys Leu Ile  
 380 385 390  
 Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro Arg Val His Leu Lys

395	400	405
Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala Leu Leu Ser Ser		
410	415	420
Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu Ala Leu Leu		
425	430	435
Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala Thr Gly		
440	445	450
Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly Ser		
455	460	465
Ala Cys Ser Thr Leu Leu Val His Leu Ile		
470	475	

<210> 80  
<211> 22  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-22  
<223> Synthetic construct.

<400> 80  
tttgcggtc accattgtct gc 22

<210> 81  
<211> 23  
<212> DNA  
<213> Homo sapiens

<220>  
<221> Artificial sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 81  
cgttaggtgac acagaagccc agg 23

<210> 82  
<211> 49  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-49  
<223> Synthetic construct.

<400> 82  
tacggcatga ccggctcctt tcctatgagg aactcccagg cactgatat 49

<210> 83  
<211> 1844

<212> DNA  
<213> Homo sapiens

<400> 83  
gacagtggag ggcagtggag aggaccgcgc tgtcctgctg tcaccaagag 50  
ctggagacac catctccac cgagagtcat ggcccattg gccctgcacc 100  
tcctcgctct cgtccccatc ctccctcagcc tggtggcctc ccaggactgg 150  
aaggctgaac gcagccaaga cccttcgag aaatgcatgc aggatcctga 200  
ctatgagcag ctgctcaagg tggtgacctg ggggctcaat cggaccctga 250  
agccccagag ggtgattgtg gttggcgctg gtgtggccgg gctggtgccc 300  
gccaagggtgc tcagcgatgc tggacacaag gtcaccatcc tggaggcaga 350  
taacaggatc gggggccgca tcttcaccta ccgggaccag aacacgggct 400  
ggattgggaa gctgggagcc atgcgcatgc ccagctctca caggatcctc 450  
cacaagctct gccagggcct ggggctcaac ctgaccaagt tcacccagta 500  
cgacaagaac acgtggacgg aggtgcacga agtgaagctg cgcaactatg 550  
tggtgagaa ggtgcccggag aagctggct acgccttgcg tccccaggaa 600  
aaggggccact cgccccaga catctaccag atggctctca accaggccct 650  
caaagacctc aaggcactgg gctgcagaaa ggcgatgaag aagtttggaa 700  
ggcacacgct cttggaatat cttctcgaaaa aggggaacct gagccggccg 750  
gccgtgcagc ttctggaga cgtgatgtcc gaggatggct tcttctatct 800  
cagcttcgccc gaggccctcc gggcccacag ctgcctcagc gacagactcc 850  
agtacagccg catcggttggt ggctgggacc tgctgcccg cgcgctgtg 900  
agctcgctgt ccgggcttgt gctgttgaac gcgcgggtgg tggcgatgac 950  
ccagggaccgg cacgatgtgc acgtgcagat cgagacctct cccccggcgc 1000  
ggaatctgaa ggtgctgaag gccgacgtgg tgctgctgac ggcgagcgg 1050  
ccggcggtga agcgcatcac cttctcgccc ccgctgcccc gccacatgca 1100  
ggaggcgctg cggaggctgc actacgtgcc ggccaccaag gtgttcctaa 1150  
gcttcggcag gcccttctgg cgcgaggagc acattgaagg cggccactca 1200  
aacaccgatc gcccgctcgcatgatttt tacccgcccgc cgcgcgaggg 1250  
cgcgctgctg ctggcctcgat acacgtggtc ggacgcggcg gcagcgatcg 1300  
ccggctttagt ccgggaagag gcgttgcgt tggcgctcga cgacgtggcg 1350

gcattgcacg ggcctgtcgt gcgccagctc tgggacggca ccggcgtcgt 1400  
 caagcggtgg gcggaggacc agcacagcca gggtggtttt gtggtacagc 1450  
 cgccggcgct ctggcaaacc gaaaaggatg actggacggt cccttatggc 1500  
 cgcacatctact ttgccggcga gcacaccgc tacccgcacg gctgggtgga 1550  
 gacggcggtc aagtccggcgc tgccgcgc catcaagatc aacagccgga 1600  
 aggggcctgc atcggacacg gccagccccg aggggcacgc atctgacatg 1650  
 gaggggcagg ggcatgtgca tgggtggcc agcagccccct cgcatgacct 1700  
 ggcaaaggaa gaaggcagcc accctccagt ccaaggccag ttatctctcc 1750  
 aaaacacgac ccacacgagg acctcgcatt aaagtatttt cgaaaaaaa 1800  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1844  
  
 <210> 84  
 <211> 567  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 84  
 Met Ala Pro Leu Ala Leu His Leu Leu Val Leu Val Pro Ile Leu  
     1                     5                         10                     15  
  
 Leu Ser Leu Val Ala Ser Gln Asp Trp Lys Ala Glu Arg Ser Gln  
     20                   25   30  
  
 Asp Pro Phe Glu Lys Cys Met Gln Asp Pro Asp Tyr Glu Gln Leu  
     35                   40   45  
  
 Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln  
     50                   55   60  
  
 Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala  
     65                   70   75  
  
 Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala  
     80                   85   90  
  
 Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn  
     95                   100   105  
  
 Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser  
    110                   115   120  
  
 His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu  
    125                   130   135  
  
 Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His  
    140                   145   150  
  
 Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys  
    155                   160   165

Leu Gly Tyr Ala Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu  
 170 175 180  
 Asp Ile Tyr Gln Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys  
 185 190 195  
 Ala Leu Gly Cys Arg Lys Ala Met Lys Lys Phe Glu Arg His Thr  
 200 205 210  
 Leu Leu Glu Tyr Leu Leu Gly Glu Gly Asn Leu Ser Arg Pro Ala  
 215 220 225  
 Val Gln Leu Leu Gly Asp Val Met Ser Glu Asp Gly Phe Phe Tyr  
 230 235 240  
 Leu Ser Phe Ala Glu Ala Leu Arg Ala His Ser Cys Leu Ser Asp  
 245 250 255  
 Arg Leu Gln Tyr Ser Arg Ile Val Gly Gly Trp Asp Leu Leu Pro  
 260 265 270  
 Arg Ala Leu Leu Ser Ser Leu Ser Gly Leu Val Leu Leu Asn Ala  
 275 280 285  
 Pro Val Val Ala Met Thr Gln Gly Pro His Asp Val His Val Gln  
 290 295 300  
 Ile Glu Thr Ser Pro Pro Ala Arg Asn Leu Lys Val Leu Lys Ala  
 305 310 315  
 Asp Val Val Leu Leu Thr Ala Ser Gly Pro Ala Val Lys Arg Ile  
 320 325 330  
 Thr Phe Ser Pro Pro Leu Pro Arg His Met Gln Glu Ala Leu Arg  
 335 340 345  
 Arg Leu His Tyr Val Pro Ala Thr Lys Val Phe Leu Ser Phe Arg  
 350 355 360  
 Arg Pro Phe Trp Arg Glu Glu His Ile Glu Gly Gly His Ser Asn  
 365 370 375  
 Thr Asp Arg Pro Ser Arg Met Ile Phe Tyr Pro Pro Pro Arg Glu  
 380 385 390  
 Gly Ala Leu Leu Leu Ala Ser Tyr Thr Trp Ser Asp Ala Ala Ala  
 395 400 405  
 Ala Phe Ala Gly Leu Ser Arg Glu Glu Ala Leu Arg Leu Ala Leu  
 410 415 420  
 Asp Asp Val Ala Ala Leu His Gly Pro Val Val Arg Gln Leu Trp  
 425 430 435  
 Asp Gly Thr Gly Val Val Lys Arg Trp Ala Glu Asp Gln His Ser  
 440 445 450  
 Gln Gly Gly Phe Val Val Gln Pro Pro Ala Leu Trp Gln Thr Glu

455	460	465
Lys Asp Asp Trp Thr Val Pro Tyr Gly Arg Ile Tyr Phe Ala Gly		
470	475	480
Glu His Thr Ala Tyr Pro His Gly Trp Val Glu Thr Ala Val Lys		
485	490	495
Ser Ala Leu Arg Ala Ala Ile Lys Ile Asn Ser Arg Lys Gly Pro		
500	505	510
Ala Ser Asp Thr Ala Ser Pro Glu Gly His Ala Ser Asp Met Glu		
515	520	525
Gly Gln Gly His Val His Gly Val Ala Ser Ser Pro Ser His Asp		
530	535	540
Leu Ala Lys Glu Glu Gly Ser His Pro Pro Val Gln Gly Gln Leu		
545	550	555
Ser Leu Gln Asn Thr Thr His Thr Arg Thr Ser His		
560	565	

<210> 85  
<211> 3316  
<212> DNA  
<213> Homo sapiens

<400> 85  
ctgacatggc ctgactcgaa acagctcaga gcagggcaga actggggaca 50  
ctctggcccg gccttctgcc tgcattggacg ctctgaagcc accctgtctc 100  
tggaggaacc acgagcgagg gaagaaggac agggactcgt gtggcagggaa 150  
gaactcagag ccggaaagcc cccattcact agaagcactg agagatgcgg 200  
ccccctcgca gggctgaat ttccctgtgc tgttcacaaa gatgctttt 250  
atcttaact ttttgtttc cccacttccg accccggcgt tgatctgcat 300  
cctgacattt ggagctgcca tcttcttggt gctgatcacc agacctcaac 350  
ccgtcttacc tcttcttgac ctgaacaatc agtctgtggg aattgagggaa 400  
ggagcacgga agggggtttc ccagaagaac aatgaccta caagttgctg 450  
cttctcagat gccaagacta tgtatgaggt tttccaaaga ggactcgctg 500  
tgtctgacaa tggccctgc ttggatata gaaaaccaa ccagccctac 550  
agatggctat cttacaaaca ggtgtctgat agagcagagt acctgggttc 600  
ctgtctttt cataaaggtt ataaatcatc accagaccag tttgtcggca 650  
tctttgctca gaataggcca gagtggatca tctccgaatt ggcttggtac 700  
acgtactcta tggtagctgt acctctgtat gacaccctgg gaccagaagc 750

catcgatcat attgtcaaca aggctgatat cgccatggtg atctgtgaca 800  
 cacccccaaaa ggcattggtg ctgataggaa atgtagagaa aggcttcacc 850  
 ccgagcctga aggtgatcat ccttatggac cccttgcgt atgacacctaa 900  
 gcaaagaggg gagaagagtg gaattgagat cttatcccta tatgatgctg 950  
 agaacctagg caaagagcac ttcagaaaac ctgtgcctcc tagcccagaa 1000  
 gacctgagcg tcatctgctt caccagtgg accacaggtg accccaaagg 1050  
 agccatgata acccatcaaa atattgtttc aaatgctgct gccttctca 1100  
 aatgtgtgga gcatgcttat gagcccactc ctgatgatgt ggccatatcc 1150  
 tacccctc tggctcatat gtttgagagg attgtacagg ctgttgtgta 1200  
 cagctgtgga gccagagttg gattcttcca agggatatt cggttgctgg 1250  
 ctgacgacat gaagactttg aagcccacat tgttccgc ggtgcctcga 1300  
 ctccctaaca gnatctacga taaggtacaa aatgaggcca agacaccctt 1350  
 gaagaagttc ttgttgaagc tggctgtttc cagtaaattc aaagagcttc 1400  
 aaaagggtat catcaggcat gatagttct gggacaagct catcttgca 1450  
 aagatccagg acagcctggg cggaaagggtt cgtgtattt tcactggagc 1500  
 tgccccatg tccacttcag tcatgacatt cttccggca gcaatggat 1550  
 gtcaggtgta tgaagcttat ggtcaaacag aatgcacagg tggctgtaca 1600  
 ttacattac ctggggactg gacatcagg cacgttgggg tgcccctggc 1650  
 ttgcaattac gtgaagctgg aagatgtggc tgacatgaac tactttacag 1700  
 tgaataatga aggagaggc tgcattcaagg gtacaaacgt gttcaaagga 1750  
 tacctgaagg accctgagaa gacacaggaa gccctggaca gtgatggctg 1800  
 gcttcacaca ggagacattt gtcgctggct cccgaatggaa actctgaaga 1850  
 tcatcgaccg taaaaagaac attttcaagc tggcccaagg agaatacatt 1900  
 gcaccagaga agatagaaaa tatctacaac aggaatcaac cagtgttaca 1950  
 aatttttgtt cacggggaga gcttacggtc atccttagta ggagtggtgg 2000  
 ttccctgacac agatgtactt ccctcattt cagccaaatct tgggggtgaag 2050  
 ggctcccttg aggaactgtg caaaaaccaa gttgtaaagg aagccatttt 2100  
 agaagacttg cagaaaattt gaaaaagaaag tggccctaaa acttttgaac 2150  
 aggtcaaagc cattttctt catccagagc cattttccat tgaaaaatggg 2200

ctcttgacac caacattgaa agcaaagcga ggagagctt ccaaatactt 2250  
tcggaccCAA attgacagcc tgtatgagca catccaggat taggataagg 2300  
tacttaagta cctgcggcc cactgtcac tgcttgtgag aaaatggatt 2350  
aaaaactatt cttacatttgc ttgccttt ctccttattt ttttttaacc 2400  
tgttaaactc taaagccata gctttgtt tatattgaga catataatgt 2450  
gtaaaacttag ttccaaata aatcaatcct gtcttccca tcttcgatgt 2500  
tgctaattttt aaggcttcag ggctactttt atcaacatgc ctgtcttcaa 2550  
gatcccagtt tatgttctgt gtccttcctc atgatttcca accttaatac 2600  
tattagtaac cacaagttca agggtcaaag ggaccctctg tgccttcttc 2650  
tttgggggtt gataaacata acttgccaaac agtctctatg cttatttaca 2700  
tcttctactg ttcaaactaa gagatttttta aattctgaaa aactgcttac 2750  
aattcatgtt ttctagccac tccacaaacc actaaaattt tagtttagc 2800  
ctatcactca tgtcaatcat atctatgaga caaatgtctc cgatgctt 2850  
ctgcgttaaat taaattgtgt actgaaggga aaagtttgcataccaaac 2900  
atttcctaaa ctctctagtt agatatctga cttgggagta taaaaatttgc 2950  
ggtctatgac atactgtcca aaaggaatgc tgttctaaa gcattattta 3000  
cagtaggaac tggggagtaa atctgttccc tacagttgc tgctgagctg 3050  
gaagctgtgg gggaggagt tgacaggtgg gcccagtgaa cttttccagt 3100  
aaatgaagca agcactgaat aaaaacctcc tgaactggga acaaagatct 3150  
acaggcaagc aagatgcccc cacaacagggc ttattttctg tgaaggaacc 3200  
aactgatctc cccccccctt ggatttagagt tcctgctcta ctttacccac 3250  
agataacaca tggtgtttctt acttgtaat gtaaagtctt taaaataaac 3300  
tattacagat aaaaaaa 3316

<210> 86  
<211> 739  
<212> PRT  
<213> Homo sapiens

<400> 86  
Met Asp Ala Leu Lys Pro Pro Cys Leu Trp Arg Asn His Glu Arg  
1 5 10 15  
Gly Lys Lys Asp Arg Asp Ser Cys Gly Arg Lys Asn Ser Glu Pro  
20 25 30

Gly Ser Pro His Ser Leu Glu Ala Leu Arg Asp Ala Ala Pro Ser  
                  35                        40                        45  
 Gln Gly Leu Asn Phe Leu Leu Leu Phe Thr Lys Met Leu Phe Ile  
                  50                        55                        60  
 Phe Asn Phe Leu Phe Ser Pro Leu Pro Thr Pro Ala Leu Ile Cys  
                  65                        70                        75  
 Ile Leu Thr Phe Gly Ala Ala Ile Phe Leu Trp Leu Ile Thr Arg  
                  80                        85                        90  
 Pro Gln Pro Val Leu Pro Leu Leu Asp Leu Asn Asn Gln Ser Val  
                  95                        100                      105  
 Gly Ile Glu Gly Gly Ala Arg Lys Gly Val Ser Gln Lys Asn Asn  
                  110                      115                      120  
 Asp Leu Thr Ser Cys Cys Phe Ser Asp Ala Lys Thr Met Tyr Glu  
                  125                      130                      135  
 Val Phe Gln Arg Gly Leu Ala Val Ser Asp Asn Gly Pro Cys Leu  
                  140                      145                      150  
 Gly Tyr Arg Lys Pro Asn Gln Pro Tyr Arg Trp Leu Ser Tyr Lys  
                  155                      160                      165  
 Gln Val Ser Asp Arg Ala Glu Tyr Leu Gly Ser Cys Leu Leu His  
                  170                      175                      180  
 Lys Gly Tyr Lys Ser Ser Pro Asp Gln Phe Val Gly Ile Phe Ala  
                  185                      190                      195  
 Gln Asn Arg Pro Glu Trp Ile Ile Ser Glu Leu Ala Cys Tyr Thr  
                  200                      205                      210  
 Tyr Ser Met Val Ala Val Pro Leu Tyr Asp Thr Leu Gly Pro Glu  
                  215                      220                      225  
 Ala Ile Val His Ile Val Asn Lys Ala Asp Ile Ala Met Val Ile  
                  230                      235                      240  
 Cys Asp Thr Pro Gln Lys Ala Leu Val Leu Ile Gly Asn Val Glu  
                  245                      250                      255  
 Lys Gly Phe Thr Pro Ser Leu Lys Val Ile Ile Leu Met Asp Pro  
                  260                      265                      270  
 Phe Asp Asp Asp Leu Lys Gln Arg Gly Glu Lys Ser Gly Ile Glu  
                  275                      280                      285  
 Ile Leu Ser Leu Tyr Asp Ala Glu Asn Leu Gly Lys Glu His Phe  
                  290                      295                      300  
 Arg Lys Pro Val Pro Pro Ser Pro Glu Asp Leu Ser Val Ile Cys  
                  305                      310                      315  
 Phe Thr Ser Gly Thr Thr Gly Asp Pro Lys Gly Ala Met Ile Thr

320	325	330
His Gln Asn Ile Val Ser Asn Ala Ala	Ala Phe Leu Lys Cys Val	
335	340	345
Glu His Ala Tyr Glu Pro Thr Pro Asp	Asp Val Ala Ile Ser Tyr	
350	355	360
Leu Pro Leu Ala His Met Phe Glu Arg	Ile Val Gln Ala Val Val	
365	370	375
Tyr Ser Cys Gly Ala Arg Val Gly Phe	Phe Gln Gly Asp Ile Arg	
380	385	390
Leu Leu Ala Asp Asp Met Lys Thr Leu	Lys Pro Thr Leu Phe Pro	
395	400	405
Ala Val Pro Arg Leu Leu Asn Arg Ile	Tyr Asp Lys Val Gln Asn	
410	415	420
Glu Ala Lys Thr Pro Leu Lys Lys Phe	Leu Leu Lys Leu Ala Val	
425	430	435
Ser Ser Lys Phe Lys Glu Leu Gln Lys	Gly Ile Ile Arg His Asp	
440	445	450
Ser Phe Trp Asp Lys Leu Ile Phe Ala	Lys Ile Gln Asp Ser Leu	
455	460	465
Gly Gly Arg Val Arg Val Ile Val Thr	Gly Ala Ala Pro Met Ser	
470	475	480
Thr Ser Val Met Thr Phe Phe Arg Ala	Ala Met Gly Cys Gln Val	
485	490	495
Tyr Glu Ala Tyr Gly Gln Thr Glu Cys	Thr Gly Gly Cys Thr Phe	
500	505	510
Thr Leu Pro Gly Asp Trp Thr Ser Gly	His Val Gly Val Pro Leu	
515	520	525
Ala Cys Asn Tyr Val Lys Leu Glu Asp	Val Ala Asp Met Asn Tyr	
530	535	540
Phe Thr Val Asn Asn Glu Gly Glu Val	Cys Ile Lys Gly Thr Asn	
545	550	555
Val Phe Lys Gly Tyr Leu Lys Asp Pro	Glu Lys Thr Gln Glu Ala	
560	565	570
Leu Asp Ser Asp Gly Trp Leu His Thr	Gly Asp Ile Gly Arg Trp	
575	580	585
Leu Pro Asn Gly Thr Leu Lys Ile Ile	Asp Arg Lys Lys Asn Ile	
590	595	600
Phe Lys Leu Ala Gln Gly Glu Tyr Ile	Ala Pro Glu Lys Ile Glu	
605	610	615

Asn Ile Tyr Asn Arg Ser Gln Pro Val Leu Gln Ile Phe Val His  
620 625 630

Gly Glu Ser Leu Arg Ser Ser Leu Val Gly Val Val Val Pro Asp  
635 640 645

Thr Asp Val Leu Pro Ser Phe Ala Ala Lys Leu Gly Val Lys Gly  
650 655 660

Ser Phe Glu Glu Leu Cys Gln Asn Gln Val Val Arg Glu Ala Ile  
665 670 675

Leu Glu Asp Leu Gln Lys Ile Gly Lys Glu Ser Gly Leu Lys Thr  
680 685 690

Phe Glu Gln Val Lys Ala Ile Phe Leu His Pro Glu Pro Phe Ser  
695 700 705

Ile Glu Asn Gly Leu Leu Thr Pro Thr Leu Lys Ala Lys Arg Gly  
710 715 720

Glu Leu Ser Lys Tyr Phe Arg Thr Gln Ile Asp Ser Leu Tyr Glu  
725 730 735

His Ile Gln Asp

<210> 87  
<211> 2725  
<212> DNA  
<213> Homo sapiens

<400> 87  
ggaggcggag gccgcggcga gccgggcccga gcagtgaggg ccctagcg 50  
gcccgagcgg ggcccggggc ccctaagcca ttcctgaagt catggctgg 100  
ccaggacatt ggtgaccgc caatccggta tggacgactg gaagcccagc 150  
ccccatca agcccttgg ggctcggaa aagcggagct ggtaccttac 200  
cttggaaat aaactgacaa accagcgggc cctgcggaga ttctgtcaga 250  
caggggccgt gctttcctg ctggtgactg tcattgtcaa tatcaagtgg 300  
atcctggaca ctcggcgagc catcagtgaa gccaatgaag acccagagcc 350  
agagcaagac tatgatgagg ccctaggccc cctggagccc ccacggcga 400  
gaggcagtgg tccccggcgg gtcctggacg tagaggtgta ttcaagtcgc 450  
agcaaagtat atgtggcagt ggatggcacc acggtgctgg aggtgagggc 500  
ccgggagcag ggccggggca tccatgtcat tgtcctcaac caggccacgg 550  
gccacgtat ggcaaacgt gtgtttgaca cgtactcacc tcatgaggat 600  
gaggccatgg tgctattcct caacatggta gcgccccggcc gagtgctcat 650

ctgcactgtc aaggatgagg gtccttcca cctcaaggac acagccaagg 700  
ctctgctgag gagcctggc agccaggctg gccctgccct gggctggagg 750  
gacacatggg cttcggtgg acgaaaagga ggtcctgtct tcggggagaa 800  
acattctaag tcacctgccc tcttccctg ggggaccca gtcctgctga 850  
agacagatgt gccattgagc tcagcagaag aggtagtgc ccactggca 900  
gacacagagc tgaaccgtcg ccggccggcgc ttctgcagca aagttgaggg 950  
ctatgaaagt gtatgcagct gcaaggaccc cacacccatc gagttcagcc 1000  
ctgaccact cccagacaac aaggcctca atgtcctgt ggctgtcatt 1050  
gcagggAACCC gaccaatta cctgtacagg atgctgcgt ctctgcttc 1100  
agcccagggg gtgttcctc agatgataac agtttcatt gacggctact 1150  
atgaggaacc catggatgtg gtggcactgt ttggctgag gggcatccag 1200  
catactccca tcagcatcaa gaatgcccgc gtgttcagc actacaaggc 1250  
cagcctcact gccactttca acctgtttcc ggaggccaag tttgctgtgg 1300  
ttctgaaaga ggacctggac attgctgtgg atttttcatt tttcctgagc 1350  
caatccatcc acctactgga ggaggatgac agcctgtact gcatctctgc 1400  
ctgaaatgac caggggtatg aacacacggc tgaggacca gcactactgt 1450  
accgtgtgga gaccatgcct gggctggcgt gggtgctcag gaggtccttg 1500  
tacaaggagg agcttgcggc caagtggcct acaccggaaa agctctggga 1550  
ttgggacatg tggatgcggc tgcctgaaca acgcgggggc cgagagtgc 1600  
tcatccctga cgtttcccgta tcctaccact ttggcatcgt cggcctcaac 1650  
atgaatggct actttcacga ggcctacttc aagaagcaca agttcaacac 1700  
ggttccaggt gtccagctca ggaatgtgga cagtctgaag aaagaagctt 1750  
atgaagtggc agttcacagg ctgctcagtg aggctgaggt tctggaccac 1800  
agcaagaacc cttgtgaaga ctctttcctg ccagacacag agggccacac 1850  
ctacgtggcc tttattcgaa tggagaaaga tggacttc accacctgga 1900  
cccagcttc caagtgcctc catatctggg acctggatgt gcgtggcaac 1950  
catcgccccc tgtggagatt gtttcggaa aagaaccact tcctgggt 2000  
gggggtccccg gttccccct actcagtgaa gaagccaccc tcagtcaccc 2050  
caatttcct ggagccaccc ccaaaggagg agggagcccc aggagcccc 2100

gaacagacat gagacctcct ccaggaccct gcggggctgg gtactgtta 2150  
ccccccaggct ggcttagccct tccctccatc ctgttaggatt ttgttagatgc 2200  
tgttagggc tggggctacc ttgtttttaa catgagactt aattactaac 2250  
tccaaggggga gggttcccct gctccaacac cccgttcctg agtaaaagt 2300  
ctatttattt acttccttgt tggagaaggg caggagagta cctggaaatc 2350  
attacgatcc ctagcagctc atcctgccct ttgaataaccc tcactttcca 2400  
ggcctggctc agaatctaac ctatttattt actgtcctga gggccttgaa 2450  
aacaggccga acctggaggg cctggatttc ttttggct ggaatgctgc 2500  
cctgagggtg gggctggctc ttactcagga aactgctgtg cccaaccat 2550  
ggacaggccc agctggggcc cacatgctga cacagactca ctcagagacc 2600  
cttagacact ggaccaggcc tcctctcagc cttcttttg tccagatttc 2650  
caaagctgga taagttggc attgattaaa aaaggagaag ccctctggga 2700  
aaaaaaaaaa aaaaaaaaaa aaaaa 2725

<210> 88  
<211> 660  
<212> PRT  
<213> Homo sapiens

<400> 88  
Met Asp Asp Trp Lys Pro Ser Pro Leu Ile Lys Pro Phe Gly Ala  
1 5 10 15  
Arg Lys Lys Arg Ser Trp Tyr Leu Thr Trp Lys Tyr Lys Leu Thr  
20 25 30  
Asn Gln Arg Ala Leu Arg Arg Phe Cys Gln Thr Gly Ala Val Leu  
35 40 45  
Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp  
50 55 60  
Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu  
65 70 75  
Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg  
80 85 90  
Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser  
95 100 105  
Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu  
110 115 120  
Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val  
125 130 135

Leu Asn Gln Ala Thr Gly His Val Met Ala Lys Arg Val Phe Asp  
                  140                         145                         150  
 Thr Tyr Ser Pro His Glu Asp Glu Ala Met Val Leu Phe Leu Asn  
                  155                         160                         165  
 Met Val Ala Pro Gly Arg Val Leu Ile Cys Thr Val Lys Asp Glu  
                  170                         175                         180  
 Gly Ser Phe His Leu Lys Asp Thr Ala Lys Ala Leu Leu Arg Ser  
                  185                         190                         195  
 Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly Trp Arg Asp Thr Trp  
                  200                         205                         210  
 Ala Phe Val Gly Arg Lys Gly Gly Pro Val Phe Gly Glu Lys His  
                  215                         220                         225  
 Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly Asp Pro Val Leu Leu  
                  230                         235                         240  
 Lys Thr Asp Val Pro Leu Ser Ser Ala Glu Glu Ala Glu Cys His  
                  245                         250                         255  
 Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg Arg Arg Phe Cys Ser  
                  260                         265                         270  
 Lys Val Glu Gly Tyr Gly Ser Val Cys Ser Cys Lys Asp Pro Thr  
                  275                         280                         285  
 Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro Asp Asn Lys Val Leu  
                  290                         295                         300  
 Asn Val Pro Val Ala Val Ile Ala Gly Asn Arg Pro Asn Tyr Leu  
                  305                         310                         315  
 Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala Gln Gly Val Ser Pro  
                  320                         325                         330  
 Gln Met Ile Thr Val Phe Ile Asp Gly Tyr Tyr Glu Glu Pro Met  
                  335                         340                         345  
 Asp Val Val Ala Leu Phe Gly Leu Arg Gly Ile Gln His Thr Pro  
                  350                         355                         360  
 Ile Ser Ile Lys Asn Ala Arg Val Ser Gln His Tyr Lys Ala Ser  
                  365                         370                         375  
 Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu Ala Lys Phe Ala Val  
                  380                         385                         390  
 Val Leu Glu Glu Asp Leu Asp Ile Ala Val Asp Phe Phe Ser Phe  
                  395                         400                         405  
 Leu Ser Gln Ser Ile His Leu Leu Glu Glu Asp Asp Ser Leu Tyr  
                  410                         415                         420  
 Cys Ile Ser Ala Trp Asn Asp Gln Gly Tyr Glu His Thr Ala Glu

425	430	435
Asp Pro Ala Leu Leu Tyr Arg Val Glu	Thr Met Pro Gly Leu Gly	
440	445	450
Trp Val Leu Arg Arg Ser Leu Tyr Lys	Glu Glu Leu Glu Pro Lys	
455	460	465
Trp Pro Thr Pro Glu Lys Leu Trp Asp	Trp Asp Met Trp Met Arg	
470	475	480
Met Pro Glu Gln Arg Arg Gly Arg Glu	Cys Ile Ile Pro Asp Val	
485	490	495
Ser Arg Ser Tyr His Phe Gly Ile Val	Gly Leu Asn Met Asn Gly	
500	505	510
Tyr Phe His Glu Ala Tyr Phe Lys Lys	His Lys Phe Asn Thr Val	
515	520	525
Pro Gly Val Gln Leu Arg Asn Val Asp	Ser Leu Lys Lys Glu Ala	
530	535	540
Tyr Glu Val Glu Val His Arg Leu Leu	Ser Glu Ala Glu Val Leu	
545	550	555
Asp His Ser Lys Asn Pro Cys Glu Asp	Ser Phe Leu Pro Asp Thr	
560	565	570
Glu Gly His Thr Tyr Val Ala Phe Ile	Arg Met Glu Lys Asp Asp	
575	580	585
Asp Phe Thr Thr Trp Thr Gln Leu Ala	Lys Cys Leu His Ile Trp	
590	595	600
Asp Leu Asp Val Arg Gly Asn His Arg	Gly Leu Trp Arg Leu Phe	
605	610	615
Arg Lys Lys Asn His Phe Leu Val Val	Gly Val Pro Ala Ser Pro	
620	625	630
Tyr Ser Val Lys Lys Pro Pro Ser Val	Thr Pro Ile Phe Leu Glu	
635	640	645
Pro Pro Pro Lys Glu Glu Gly Ala Pro	Gly Ala Pro Glu Gln Thr	
650	655	660

<210> 89  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 89

gatggcaaaa cgtgttgc acacg 25  
<210> 90  
<211> 22  
<212> DNA  
<213> Artificial  
  
<220>  
<221> Artificial sequence  
<222> 1-22  
<223> Synthetic construct.  
  
<400> 90  
cctcaaccag gccacgggcc ac 22  
  
<210> 91  
<211> 24  
<212> DNA  
<213> Artificial  
  
<220>  
<221> Artificial sequence  
<222> 1-24  
<223> Synthetic construct.  
  
<400> 91  
cccaggcaga gatgcgtac aggc 24  
  
<210> 92  
<211> 26  
<212> DNA  
<213> Artificial  
  
<220>  
<221> Artificial sequence  
<222> 1-26  
<223> Synthetic construct.  
  
<400> 92  
cctccagtag gtggatggat tggctc 26  
  
<210> 93  
<211> 47  
<212> DNA  
<213> Artificial  
  
<220>  
<221> Artificial sequence  
<222> 1-47  
<223> Synthetic construct.  
  
<400> 93  
ctcacctcat gaggatgagg ccatggtgct attcctcaac atggtag 47  
  
<210> 94  
<211> 3037  
<212> DNA  
<213> Homo sapiens

<400> 94  
cggacgcgtg ggctgctgg gggaggcct aaagaactgg aaagcccact 50  
ctcttggAAC caccacaccc tttaaAGAA cctaAGCACC atttaAGCC 100  
actggaaATT ttttgtag tggttgtggg tgaataaAGG agggcagaat 150  
ggatgatttc atctccatta gcctgctgtc tctggctatg ttggtggat 200  
gttacgtggc cggaatcatt cccttggctg ttaatttctc agaggaacga 250  
ctgaagctgg tgactgtttt gggtgctggc cttctctgtg gaactgctct 300  
ggcagtcatc gtgcctgaag gagtacatgc cctttatgaa gatattctt 350  
agggaaaaca ccaccaagca agtgaardac ataatgtat tgcatacagac 400  
aaagcagcag aaaaatcagt tgtccatgaa catgagcaca gccacgacca 450  
cacacagctg catgcctata ttggtgtttc cctcgttctg ggcttcgttt 500  
tcatgttgc ggtggaccag attggtaact cccatgtgca ttctactgac 550  
gatccagaag cagcaaggTC tagcaattcc aaaatcacca ccacgctggg 600  
tctgggtgtc catgctgcag ctgatgggt tgctttggc gcagcagcat 650  
ctacttcaca gaccagtgtc cagttaatgg tgtttggc aatcatgcta 700  
cataaggcac cagctgcttt tggactgggt tccttcttga tgcatgctgg 750  
cttagagcgg aatcgaatca gaaagcactt gctggtcttt gcattggcag 800  
caccagttat gtccatggtg acatacttag gactgagtaa gagcagtaaa 850  
gaagcccttt cagaggtgaa cgccacggg gttccatgc ttttctctgc 900  
cgggacattt cttaatgttg ccacagtaca tgcctccct gaggtggcgc 950  
gaataggGCa cagccacaag cccgatGCCA cgggaggag aggccTCAGC 1000  
cgcctggaaag tggcagccct gttctgggt tgcctcatcc ctctcatcct 1050  
gtcagtagga caccagcatt aaatgttcaa ggtccagcct tggccagg 1100  
ccgtttGCCA tccagtgaga acagccggca cgtgacagct actcaacttcc 1150  
tcagtctctt gtctcacctt ggcacatctt acatgttattc cttagtcca 1200  
gaggggaggt gaggtaaaa cctgagtaat ggaaaagctt ttagagtaga 1250  
aacacatttA cgttgcagtt agctatacAC atccccattgt gttatcttt 1300  
aaaaggccct tgacatTTG cgttttaata tttctcttAA ccctattctc 1350  
agggaaAGATG gaatttagtt ttaaggaaaa gaggagaact tcataactcac 1400  
aatgaaatAG tgattatgaa aatacagtgt tctgttaattt agctatgtct 1450

ctttcttctt agtttagagg ctctgctact ttatccattg attttaaca 1500  
tggttcccac catgtaagac tggtgcttta gcatctatgc cacatgcgtt 1550  
gatggaaggt catagcaccc actcacttag atgctaaagg tgattctagt 1600  
taatctggga ttagggtcag gaaaatgata gcaagacaca ttgaaagctc 1650  
tctttatact caaaagagat atccattgaa aaggatgtc tagagggatt 1700  
taaacagctc ctttggcacg tgcctctctg aatccagcct gccattccat 1750  
caaatggagc aggagaggtg ggaggagctt ctaaagaggt gactggtatt 1800  
ttgttagcatt ctttgtcaag ttctccttgcagaataacct gtctccacat 1850  
tcctagagag gagccaagtt ctagtagttt cagttctagg ctttccttca 1900  
agaacagtca gatcacaaag tgtctttgaa attaaggaa tattaaattt 1950  
taagtgattt ttggatggtt attgatatct ttgttagtagc tttttttaaa 2000  
agactaccaa aatgtatggt tgtccttttt ttttgggggg 2050  
attatttctc ttagcagatc agcaatccct ctagggacct aaatactagg 2100  
tcagctttgg cgacactgtg tcttcacaca taaccacctg tagcaagatg 2150  
gatcataaat gagaagtgtt tgcctattga tttaaagctt attggatca 2200  
tgtctttgt ctcttcgtct tttctttgtctttctaa cttttccctc 2250  
tagcctctcc tcgccacaat ttgctgctta ctgctgggtt taatatttgt 2300  
gtgggatgaa ttcttatcag gacaaccact tctcgaactg taataatgaa 2350  
gataataata tctttattct ttatcccctt caaagaaatt acctttgtgt 2400  
caaatgccgc tttgttgagc cttaaaata ccacccctc atgtgtaaat 2450  
tgacacaatc actaatctgg taatttaaac aattgagata gcaaaagtgt 2500  
ttaacagact aggataattt tttttcata ttgccaataa tttttgtaaa 2550  
ccctgtcttg tcaaataagt gtataatatt gtattattaa tttatttta 2600  
ctttctatac cattcaaaa cacattacac taagggggaa ccaagactag 2650  
tttcttcagg gcagtggacg tagtagttttaaaaaacgtt ttctatgacg 2700  
cataagctag catgcctatg atttatttcc ttcatgaatt tgcactgga 2750  
tcagcagctg tggaaataaa gcttgtgagc cctctgctgg ccacagttag 2800  
gaaaatggtagca caaataggat acagttgtat gtagtcattt gcaacaattt 2850  
catacaattt tactaccaag agaaggataa gtaggaaag tccaaatgac 2900

ttccttgatt ggatgttaac agctgactgg tgtgagactt gaggtttcat 2950  
 ctagccttc aaaactataat ggtgcctag attctctctg gaaactgact 3000  
 ttgtcaaata aatagcagat tgttagtgtca aaaaaaa 3037  
  
 <210> 95  
 <211> 307  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 95  
 Met Asp Asp Phe Ile Ser Ile Ser Leu Leu Ser Leu Ala Met Leu  
     1               5                  10                 15  
  
 Val Gly Cys Tyr Val Ala Gly Ile Ile Pro Leu Ala Val Asn Phe  
     20                 25                 30  
  
 Ser Glu Glu Arg Leu Lys Leu Val Thr Val Leu Gly Ala Gly Leu  
     35                 40                 45  
  
 Leu Cys Gly Thr Ala Leu Ala Val Ile Val Pro Glu Gly Val His  
     50                 55                 60  
  
 Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser  
     65                 70                 75  
  
 Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser  
     80                 85                 90  
  
 Val Val His Glu His Ser His Asp His Thr Gln Leu His  
     95                 100                105  
  
 Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu  
   110                 115                120  
  
 Leu Val Asp Gln Ile Gly Asn Ser His Val His Ser Thr Asp Asp  
   125                 130                135  
  
 Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu  
   140                 145                150  
  
 Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala  
   155                 160                165  
  
 Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val  
   170                 175                180  
  
 Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser  
   185                 190                195  
  
 Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His  
   200                 205                210  
  
 Leu Leu Val Phe Ala Leu Ala Ala Pro Val Met Ser Met Val Thr  
   215                 220                225  
  
 Tyr Leu Gly Leu Ser Lys Ser Ser Lys Glu Ala Leu Ser Glu Val

230	235	240
Asn Ala Thr Gly Val Ala Met Leu Phe Ser Ala Gly Thr Phe Leu		
245	250	255
Tyr Val Ala Thr Val His Val Leu Pro Glu Val Gly Gly Ile Gly		
260	265	270
His Ser His Lys Pro Asp Ala Thr Gly Gly Arg Gly Leu Ser Arg		
275	280	285
Leu Glu Val Ala Ala Leu Val Leu Gly Cys Leu Ile Pro Leu Ile		
290	295	300
Leu Ser Val Gly His Gln His		
305		

<210> 96  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 96  
gttgtgggtg aataaaggag ggcag 25

<210> 97  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 97  
ctgtgctcat gttcatggac aactg 25

<210> 98  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 98  
ggatgatttc atctccatta gcctgctgtc tctggctatg ttgggtggat 50

<210> 99  
<211> 1429

<212> DNA  
<213> Homo sapiens

<400> 99  
gctcgaggcc ggcggcggcg ggagagcgac ccgggcggcc tcgttagcggg 50  
cccccgatc cccgagtggc ggccggagcc tcgaaaagag attctcagcg 100  
ctgattttga gatgatgggc ttggaaacg ggcgtcgcag catgaagtgc 150  
ccgcccctcg tgctggccgc cctggtgcc tcgtcatcatcg tcttgggctt 200  
caactactgg attgcgagct cccggagcgt ggacctccag acacggatca 250  
tggagctgga aggcaagggtc cgcaggcggt ctgcagagag aggcgccgtg 300  
gagctgaaga agaacgagtt ccagggagag ctggagaagc agcgggagca 350  
gcttgacaaa atccagtcca gccacaactt ccagctggag agcgtcaaca 400  
agctgtacca ggacgaaaag gcggtttgg tgaataacat caccacaggt 450  
gagaggctca tccgagtgtc gcaagaccag ttaaagaccc tgcagaggaa 500  
ttacggcagg ctgcagcagg atgtcctcca gtttcagaag aaccagacca 550  
acctggagag gaagttctcc tacgacactga gccagtgcatt caatcagatg 600  
aaggaggtga aggaacagtg tgaggagcga atagaagagg tcaccaaaaa 650  
gggaaatgaa gctgtagctt ccagagacct gagtggaaac aacgaccaga 700  
gacagcagct ccaagccctc agtgagcctc agcccaggct gcaggcagca 750  
ggcctgccac acacagaggt gccacaaggg aagggaaacg tgcttgtaa 800  
cagcaagtcc cagacaccag cccccagttc cgaagtggtt ttggattcaa 850  
agagacaagt tgagaaagag gaaaccaatg agatccaggt ggtgaatgag 900  
gagcctcaga gggacaggct gccgcaggag ccaggccggg agcaggtggt 950  
ggaagacaga cctgttaggtg gaagaggctt cgggggagcc ggagaactgg 1000  
gccagacccc acaggtgcag gctgccctgt cagtgcacca gaaaaatcca 1050  
gagatggagg gccctgagcg agaccagctt gtcatccccg acggacagga 1100  
ggaggaggcag gaagctgccc gggaaaggag aaaccagcag aaactgagag 1150  
gagaagatga ctacaacatg gatgaaaatg aagcagaatc tgagacagac 1200  
aagcaagcag ccctggcagg gaatgacaga aacatagatg ttttaatgt 1250  
tgaagatcag aaaagagaca ccataaattt acttgatcag cgtgaaaagc 1300  
ggaatcatac actctgaatt gaactggaat cacatattc acaacaggc 1350

cgaagagatg actataaaat gttcatgagg gactgaatac tgaaaactgt 1400  
 gaaatgtact aaataaaatg tacatctga 1429  
 <210> 100  
 <211> 401  
 <212> PRT  
 <213> Homo sapiens  
 <400> 100  
 Met Met Gly Leu Gly Asn Gly Arg Arg Ser Met Lys Ser Pro Pro  
 1 5 10 15  
 Leu Val Leu Ala Ala Leu Val Ala Cys Ile Ile Val Leu Gly Phe  
 20 25 30  
 Asn Tyr Trp Ile Ala Ser Ser Arg Ser Val Asp Leu Gln Thr Arg  
 35 40 45  
 Ile Met Glu Leu Glu Gly Arg Val Arg Arg Ala Ala Ala Glu Arg  
 50 55 60  
 Gly Ala Val Glu Leu Lys Lys Asn Glu Phe Gln Gly Glu Leu Glu  
 65 70 75  
 Lys Gln Arg Glu Gln Leu Asp Lys Ile Gln Ser Ser His Asn Phe  
 80 85 90  
 Gln Leu Glu Ser Val Asn Lys Leu Tyr Gln Asp Glu Lys Ala Val  
 95 100 105  
 Leu Val Asn Asn Ile Thr Thr Gly Glu Arg Leu Ile Arg Val Leu  
 110 115 120  
 Gln Asp Gln Leu Lys Thr Leu Gln Arg Asn Tyr Gly Arg Leu Gln  
 125 130 135  
 Gln Asp Val Leu Gln Phe Gln Lys Asn Gln Thr Asn Leu Glu Arg  
 140 145 150  
 Lys Phe Ser Tyr Asp Leu Ser Gln Cys Ile Asn Gln Met Lys Glu  
 155 160 165  
 Val Lys Glu Gln Cys Glu Glu Arg Ile Glu Glu Val Thr Lys Lys  
 170 175 180  
 Gly Asn Glu Ala Val Ala Ser Arg Asp Leu Ser Glu Asn Asn Asp  
 185 190 195  
 Gln Arg Gln Gln Leu Gln Ala Leu Ser Glu Pro Gln Pro Arg Leu  
 200 205 210  
 Gln Ala Ala Gly Leu Pro His Thr Glu Val Pro Gln Gly Lys Gly  
 215 220 225  
 Asn Val Leu Gly Asn Ser Lys Ser Gln Thr Pro Ala Pro Ser Ser  
 230 235 240

Glu Val Val Leu Asp Ser Lys Arg Gln Val Glu Lys Glu Glu Thr  
 245 250 255  
 Asn Glu Ile Gln Val Val Asn Glu Glu Pro Gln Arg Asp Arg Leu  
 260 265 270  
 Pro Gln Glu Pro Gly Arg Glu Gln Val Val Glu Asp Arg Pro Val  
 275 280 285  
 Gly Gly Arg Gly Phe Gly Gly Ala Gly Glu Leu Gly Gln Thr Pro  
 290 295 300  
 Gln Val Gln Ala Ala Leu Ser Val Ser Gln Glu Asn Pro Glu Met  
 305 310 315  
 Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro Asp Gly Gln Glu  
 320 325 330  
 Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn Gln Gln Lys Leu  
 335 340 345  
 Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala Glu Ser  
 350 355 360  
 Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn Ile  
 365 370 375  
 Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr Ile Asn Leu  
 380 385 390  
 Leu Asp Gln Arg Glu Lys Arg Asn His Thr Leu  
 395 400

<210> 101  
 <211> 3671  
 <212> DNA  
 <213> Homo sapiens

<400> 101  
 ggatgcagaa agcctcagtg ttgctttcc tggcctgggt ctgcttcctc 50  
 ttctacgctg gcattgccct cttcaccagt ggcttctgc tcacccgttt 100  
 ggagctcacc aaccatagca gctgccaaga gccccccaggc cctgggtccc 150  
 tgccatgggg gagccaaggg aaacctgggg cctgctggat ggcttcccgaa 200  
 ttttcgcggg ttgtgttgt gctgatacat gctctgcgtt ttgacttcgc 250  
 ccagccccag cattcacacg tgccttagaga gcctcctgtc tccctaccct 300  
 tcctggccaa actaagctcc ttgcagagga tcctggagat tcagccccac 350  
 catgccccggc tctaccgatc tcaggttgac cctccttacca ccaccatgca 400  
 gcgccctcaag gccctcacca ctggctcaact gcctaccttt attgatgctg 450  
 gtagtaactt cgccagccac gccatagtgg aagacaatct cattaagcag 500

ctcaccagtg caggaaggcg tgtagtcttc atggagatg atacctgaa 550  
agacctttc cctggtgctt tctccaaagc tttcttcttc ccattctca 600  
atgtcagaga cctagacaca gtggacaatg gcattctgga acacctctac 650  
cccaccatgg acagtggta atgggacgtg ctgattgctc acttcctggg 700  
tgtggaccac tgtggccaca agcatggccc tcaccaccct gaaatggcca 750  
agaaaacttag ccagatggac caggtgatcc agggacttgt ggagcgtctg 800  
gagaatgaca cactgctggt agtggctgg gaccatggga tgaccacaaa 850  
tggagaccat ggaggggaca gtgagctgga ggtctcagct gctctttc 900  
tgtatagccc cacagcagtc ttccccagca cccaccaga ggagccagag 950  
gtgattcctc aagttagcct tgtgccacg ctggccctgc tgctggcct 1000  
gcccatccca tttggaaata tcgggaaagt gatggctgag ctattctcag 1050  
ggggtgagga ctcccagccc cactcctctg cttagccca agcctcagct 1100  
ctccatctca atgctcagca ggtgtccca tttcttcata cctactcagc 1150  
tgctactcag gaccttcaag ctaaggagct tcattcagctg cagaacctct 1200  
tctccaaggc ctctgctgac taccagtggc ttctccagag ccccaagggg 1250  
gctgaggcga cactgccac tgtgattgct gagctgcagc agttcctgcg 1300  
gggagctcgg gccatgtgca tcgagtcttg ggctcggttc tctctggtcc 1350  
gcatggcggg gggtaactgct ctctggctg ctccctgctt tatctgcctg 1400  
ctggcatctc agtgggcaat atccccaggc tttccattct gccctctact 1450  
cctgacacct gtggcctggg gcctgggtgg ggccatagcg tatgctggac 1500  
tcctggaaac tattgagctg aagctagatc tagtgcttct aggggctgtg 1550  
gctgcagtga gctcattcct ccctttctg tggaaaggct gggctggctg 1600  
ggggtccaag aggccccctgg caaccctgtt tcccatccct gggcccggtcc 1650  
tgttactcct gctgttcgc ttggctgtgt tcttctctga tagtttgtt 1700  
gtagctgagg ccagggccac ccccttcctt ttgggctcat tcattcctgct 1750  
cctggttgtc cagttcact gggagggcca gctgcttcca cctaagctac 1800  
tcacaatgcc ccgccttggc acttcagcca caacaaaccc cccacggcac 1850  
aatggtgcat atgccctgag gcttggaaatt gggttgcttt tatgtacaag 1900  
gctagctggg cttttcatc gttgccctga agagacacct gttgccact 1950

cctctccctg gctgagtcct ctggcatcca tgggggtgg tcgagccaag 2000  
aatttatggt atggagcttg tgtggcggcg ctggggccc tgtagctgc 2050  
cgtgcgcttg tggctcgcc gctatggtaa tctcaagagc cccgagccac 2100  
ccatgcttttgtgcgtgg ggactgcccc taatggcatt gggtaactgct 2150  
gcctactggg cattggcgtc gggggcagat gaggctccc cccgtctccg 2200  
ggtcctggtc tctggggcat ccatggtgc gcctcggct gtagcaggc 2250  
tggctgcttc agggctcgcg ctgctgcct ggaaggctgt gacagtgcgt 2300  
gtgaaggctg gggcaggcgc tccaaggacc aggactgtcc tcactccctt 2350  
ctcaggcccc cccacttctc aagctgaccc ggattatgtg gtccctcaaa 2400  
tctaccgaca catgcaggag gagttccggg gccggtaga gaggacaaa 2450  
tctcagggtc ccctgactgt ggctgcttat cagttggga gtgtctactc 2500  
agctgctatg gtcacagccc tcaccctgtt ggccttccca cttctgctgt 2550  
tgcatgcgga gcgcatacgc cttgtgttcc tgcttctgtt tctgcagagc 2600  
ttccttctcc tacatctgct tgctgctggg ataccgtca ccaccctgg 2650  
tcctttact gtgccatggc aggcaactc ggcttggcc ctcataggcca 2700  
cacagaccc ttactccaca ggccaccaggc ctgtcttcc agccatccat 2750  
tggcatgcag cttcgtggg attcccaagag ggtcatggct cctgtacttg 2800  
gctgcctgct ttgctagtgg gagccaacac cttgcctcc cacctcctct 2850  
ttgcagtagg ttgccactg ctcctgctct ggccttccct gtgtgagagt 2900  
caagggctgc ggaagagaca gcagccccc gggaatgaag ctgatgccag 2950  
agtcaaaaaa gaggaggaag aggagccact gatggagatg cggctccggg 3000  
atgcgcctca gcacttctat gcagcactgc tgcaagtcggg cctcaagttac 3050  
ctcttatcc ttggattca gattctggcc tggccttgg cagcctccat 3100  
ccttcgcagg catctcatgg tctggaaagt gtttgcctt aagttcatat 3150  
ttgaggctgt gggcttcatt gtgagcagcg tggacttct cctggcata 3200  
gctttggta tgagagtgg tggctgtg agctcctggt tcaggcagct 3250  
atttctggcc cagcagaggt agcctagtct gtgattactg gcacttggct 3300  
acagagatg ctggagaaca gtgttagcctg gcctgtacag gtactggatg 3350  
atctgcaaga caggctcagc catactctta ctatcatgca gccagggccc 3400

gctgacatct aggacttcat tattctataa ttcaggacca cagtggagta 3450  
tgatccctaa ctcctgattt gatatgcattt gagggacaag gggggcggtc 3500  
tccgaagtgg aataaaaatag gccgggcgtg gtgacttgca cctataatcc 3550  
cagcactttggagggcagag gtgggaggat tgcttggtcc caggagttca 3600  
agaccagcct gtggaacata acaagacccc gtctctacta tttaaaaaaa 3650  
agtgtataaa aatgataata t 3671

<210> 102

<211> 1089

<212> PRT

<213> Homo sapiens

<400> 102

Met	Gln	Lys	Ala	Ser	Val	Leu	Leu	Phe	Leu	Ala	Trp	Val	Cys	Phe
1					5				10				15	
Leu	Phe	Tyr	Ala	Gly	Ile	Ala	Leu	Phe	Thr	Ser	Gly	Phe	Leu	Leu
					20				25				30	
Thr	Arg	Leu	Glu	Leu	Thr	Asn	His	Ser	Ser	Cys	Gln	Glu	Pro	Pro
					35				40				45	
Gly	Pro	Gly	Ser	Leu	Pro	Trp	Gly	Ser	Gln	Gly	Lys	Pro	Gly	Ala
					50				55				60	
Cys	Trp	Met	Ala	Ser	Arg	Phe	Ser	Arg	Val	Val	Leu	Val	Leu	Ile
					65				70				75	
Asp	Ala	Leu	Arg	Phe	Asp	Phe	Ala	Gln	Pro	Gln	His	Ser	His	Val
					80				85				90	
Pro	Arg	Glu	Pro	Pro	Val	Ser	Leu	Pro	Phe	Leu	Gly	Lys	Leu	Ser
					95				100				105	
Ser	Leu	Gln	Arg	Ile	Leu	Glu	Ile	Gln	Pro	His	His	Ala	Arg	Leu
					110				115				120	
Tyr	Arg	Ser	Gln	Val	Asp	Pro	Pro	Thr	Thr	Thr	Met	Gln	Arg	Leu
					125				130				135	
Lys	Ala	Leu	Thr	Thr	Gly	Ser	Leu	Pro	Thr	Phe	Ile	Asp	Ala	Gly
					140				145				150	
Ser	Asn	Phe	Ala	Ser	His	Ala	Ile	Val	Glu	Asp	Asn	Leu	Ile	Lys
					155				160				165	
Gln	Leu	Thr	Ser	Ala	Gly	Arg	Arg	Val	Val	Phe	Met	Gly	Asp	Asp
					170				175				180	
Thr	Trp	Lys	Asp	Leu	Phe	Pro	Gly	Ala	Phe	Ser	Lys	Ala	Phe	Phe
					185				190				195	
Phe	Pro	Ser	Phe	Asn	Val	Arg	Asp	Leu	Asp	Thr	Val	Asp	Asn	Gly

200	205	210
Ile Leu Glu His Leu Tyr Pro Thr Met Asp Ser Gly Glu Trp Asp		
215	220	225
Val Leu Ile Ala His Phe Leu Gly Val Asp His Cys Gly His Lys		
230	235	240
His Gly Pro His His Pro Glu Met Ala Lys Lys Leu Ser Gln Met		
245	250	255
Asp Gln Val Ile Gln Gly Leu Val Glu Arg Leu Glu Asn Asp Thr		
260	265	270
Leu Leu Val Val Ala Gly Asp His Gly Met Thr Thr Asn Gly Asp		
275	280	285
His Gly Gly Asp Ser Glu Leu Glu Val Ser Ala Ala Leu Phe Leu		
290	295	300
Tyr Ser Pro Thr Ala Val Phe Pro Ser Thr Pro Pro Glu Glu Pro		
305	310	315
Glu Val Ile Pro Gln Val Ser Leu Val Pro Thr Leu Ala Leu Leu		
320	325	330
Leu Gly Leu Pro Ile Pro Phe Gly Asn Ile Gly Glu Val Met Ala		
335	340	345
Glu Leu Phe Ser Gly Gly Glu Asp Ser Gln Pro His Ser Ser Ala		
350	355	360
Leu Ala Gln Ala Ser Ala Leu His Leu Asn Ala Gln Gln Val Ser		
365	370	375
Arg Phe Leu His Thr Tyr Ser Ala Ala Thr Gln Asp Leu Gln Ala		
380	385	390
Lys Glu Leu His Gln Leu Gln Asn Leu Phe Ser Lys Ala Ser Ala		
395	400	405
Asp Tyr Gln Trp Leu Leu Gln Ser Pro Lys Gly Ala Glu Ala Thr		
410	415	420
Leu Pro Thr Val Ile Ala Glu Leu Gln Gln Phe Leu Arg Gly Ala		
425	430	435
Arg Ala Met Cys Ile Glu Ser Trp Ala Arg Phe Ser Leu Val Arg		
440	445	450
Met Ala Gly Gly Thr Ala Leu Leu Ala Ala Ser Cys Phe Ile Cys		
455	460	465
Leu Leu Ala Ser Gln Trp Ala Ile Ser Pro Gly Phe Pro Phe Cys		
470	475	480
Pro Leu Leu Leu Thr Pro Val Ala Trp Gly Leu Val Gly Ala Ile		
485	490	495

Ala Tyr Ala Gly Leu Leu Gly Thr Ile Glu Leu Lys Leu Asp Leu  
 500 505 510  
 Val Leu Leu Gly Ala Val Ala Val Ser Ser Phe Leu Pro Phe  
 515 520 525  
 Leu Trp Lys Ala Trp Ala Gly Trp Gly Ser Lys Arg Pro Leu Ala  
 530 535 540  
 Thr Leu Phe Pro Ile Pro Gly Pro Val Leu Leu Leu Leu Leu Phe  
 545 550 555  
 Arg Leu Ala Val Phe Phe Ser Asp Ser Phe Val Val Ala Glu Ala  
 560 565 570  
 Arg Ala Thr Pro Phe Leu Leu Gly Ser Phe Ile Leu Leu Leu Val  
 575 580 585  
 Val Gln Leu His Trp Glu Gly Gln Leu Leu Pro Pro Lys Leu Leu  
 590 595 600  
 Thr Met Pro Arg Leu Gly Thr Ser Ala Thr Thr Asn Pro Pro Arg  
 605 610 615  
 His Asn Gly Ala Tyr Ala Leu Arg Leu Gly Ile Gly Leu Leu Leu  
 620 625 630  
 Cys Thr Arg Leu Ala Gly Leu Phe His Arg Cys Pro Glu Glu Thr  
 635 640 645  
 Pro Val Cys His Ser Ser Pro Trp Leu Ser Pro Leu Ala Ser Met  
 650 655 660  
 Val Gly Gly Arg Ala Lys Asn Leu Trp Tyr Gly Ala Cys Val Ala  
 665 670 675  
 Ala Leu Val Ala Leu Leu Ala Ala Val Arg Leu Trp Leu Arg Arg  
 680 685 690  
 Tyr Gly Asn Leu Lys Ser Pro Glu Pro Pro Met Leu Phe Val Arg  
 695 700 705  
 Trp Gly Leu Pro Leu Met Ala Leu Gly Thr Ala Ala Tyr Trp Ala  
 710 715 720  
 Leu Ala Ser Gly Ala Asp Glu Ala Pro Pro Arg Leu Arg Val Leu  
 725 730 735  
 Val Ser Gly Ala Ser Met Val Leu Pro Arg Ala Val Ala Gly Leu  
 740 745 750  
 Ala Ala Ser Gly Leu Ala Leu Leu Leu Trp Lys Pro Val Thr Val  
 755 760 765  
 Leu Val Lys Ala Gly Ala Gly Ala Pro Arg Thr Arg Thr Val Leu  
 770 775 780  
 Thr Pro Phe Ser Gly Pro Pro Thr Ser Gln Ala Asp Leu Asp Tyr

785	790	795
Val Val Pro Gln Ile Tyr Arg His Met	Gln Glu Glu Phe Arg	Gly
800	805	810
Arg Leu Glu Arg Thr Lys Ser Gln Gly	Pro Leu Thr Val Ala Ala	
815	820	825
Tyr Gln Leu Gly Ser Val Tyr Ser Ala Ala	Met Val Thr Ala Leu	
830	835	840
Thr Leu Leu Ala Phe Pro Leu Leu Leu	His Ala Glu Arg Ile	
845	850	855
Ser Leu Val Phe Leu Leu Leu Phe Leu	Gln Ser Phe Leu Leu	
860	865	870
His Leu Leu Ala Ala Gly Ile Pro Val	Thr Thr Pro Gly Pro	Phe
875	880	885
Thr Val Pro Trp Gln Ala Val Ser Ala	Trp Ala Leu Met Ala	Thr
890	895	900
Gln Thr Phe Tyr Ser Thr Gly His Gln	Pro Val Phe Pro Ala	Ile
905	910	915
His Trp His Ala Ala Phe Val Gly Phe	Pro Glu Gly His Gly	Ser
920	925	930
Cys Thr Trp Leu Pro Ala Leu Leu Val	Gly Ala Asn Thr Phe	Ala
935	940	945
Ser His Leu Leu Phe Ala Val Gly Cys	Pro Leu Leu Leu Leu	Trp
950	955	960
Pro Phe Leu Cys Glu Ser Gln Gly Leu Arg	Lys Arg Gln Gln	Pro
965	970	975
Pro Gly Asn Glu Ala Asp Ala Arg Val	Arg Pro Glu Glu Glu	
980	985	990
Glu Pro Leu Met Glu Met Arg Leu Arg Asp	Ala Pro Gln His Phe	
995	1000	1005
Tyr Ala Ala Leu Leu Gln Leu Gly	Leu Lys Tyr Leu Phe Ile Leu	
1010	1015	1020
Gly Ile Gln Ile Leu Ala Cys Ala Leu Ala Ala	Ser Ile Leu Arg	
1025	1030	1035
Arg His Leu Met Val Trp Lys Val Phe Ala	Pro Lys Phe Ile Phe	
1040	1045	1050
Glu Ala Val Gly Phe Ile Val Ser Ser Val	Gly Leu Leu Leu Gly	
1055	1060	1065
Ile Ala Leu Val Met Arg Val Asp Gly Ala Val Ser Ser Trp	Phe	
1070	1075	1080

Arg Gln Leu Phe Leu Ala Gln Gln Arg  
1085

<210> 103  
<211> 1743  
<212> DNA  
<213> Homo sapiens

<400> 103  
tgccgctgcc gcccgtgctg ctgttgcctc tggcgccgc ttggggacgg 50  
gcagttccct gtgtctctgg tggttgccct aaacctgcaa acatcacctt 100  
cttatccatc aacatgaaga atgtcctaca atggactcca ccagagggtc 150  
ttcaaggagt taaagttact tacactgtgc agtatttcat cacaattgg 200  
ccccaccagag gtggcactga ctacagatga gaagtccatt tctgttgcc 250  
tgacagctcc agagaagtgg aagagaaatc cagaagacct tcctgttcc 300  
atgcaacaaa tatactccaa tctgaagtat aacgtgtctg tggtaatac 350  
taaatcaaac agaacgtggt cccagtgtgt gaccaaccac acgctgggtc 400  
tcacctggct ggagccgaac actctttact gcgtacacgt ggagtccctc 450  
gtccccagggc cccctcgccg tgctcagcct tctgagaagc agtgtgccag 500  
gactttgaaa gatcaatcat cagagttcaa ggctaaaatc atcttctgg 550  
atgtttgcc catatctatt accgtgttcc tttttctgt gatggctat 600  
tccatctacc gatatatcca cggtggcaaa gagaaacacc cagcaaattt 650  
gattttgatt tatggaaatg aatttgacaa aagattctt gtgcctgctg 700  
aaaaaatcgt gattaacttt atcaccctca atatctcgga tgattctaaa 750  
atttctcatc aggatatgag tttactggga aaaagcagtg atgtatccag 800  
ccttaatgat cctcagccca gcgggAACCTT gaggccccctt caggaggaag 850  
aggaggtgaa acatttaggg tatgcttcgc atttgatggaa aatttttgt 900  
gactctgaag aaaacacgga aggtacttct ctcacccagc aagagtccct 950  
cagcagaaca atacccccgg ataaaacagt cattgaatat gaatatgatg 1000  
tcagaaccac tgacatttgt gcggggcctg aagagcagga gctcagttg 1050  
caggaggagg tgtccacaca aggaacattt ttggagtcgc aggcagcgtt 1100  
ggcagtcttg ggcccgcaaa cgttacagta ctcatacacc cctcagctcc 1150  
aagacttaga cccccctggcg caggagcaca cagactcgga ggagggccg 1200  
gaggaagagc catcgacgac cctggtcgac tggatcccc aaactggcag 1250

gctgtgtatt cttcgctgt ccagcttcga ccaggattca gagggtgcg 1300  
agccttctga gggggatggg ctcggagagg agggtcttct atctagactc 1350  
tatgaggagc cggccccaaga caggccacca ggagaaaatg aaacctatct 1400  
catgcaattc atggaggaat ggggttata tgtgcagatg gaaaactgat 1450  
gccaacactt cttttgcct tttgtttct gtgcaaaca gtgagtcacc 1500  
ccttgatcc cagccataaa gtacctggg tgaaagaagt ttttccagt 1550  
ttgtcagtgt ctgtgagaat tacttatttc ttttctctat tctcatagca 1600  
cgtgtgtat ttgttcatgc atgttaggtct cttaacaatg atggtgggcc 1650  
tctggagtcc aggggctggc cggttgcct atgcagagaa agcagtcaat 1700  
aaatgtttgc cagactgggt gcagaattta ttcaggtggg tgt 1743

<210> 104

<211> 442

<212> PRT

<213> Homo sapiens

<400> 104

Met	Ser	Tyr	Asn	Gly	Leu	His	Gln	Arg	Val	Phe	Lys	Glu	Leu	Lys
1				5					10				15	
Leu	Leu	Thr	Leu	Cys	Ser	Ile	Ser	Ser	Gln	Ile	Gly	Pro	Pro	Glu
				20						25				30
Val	Ala	Leu	Thr	Thr	Asp	Glu	Lys	Ser	Ile	Ser	Val	Val	Leu	Thr
					35				40					45
Ala	Pro	Glu	Lys	Trp	Lys	Arg	Asn	Pro	Glu	Asp	Leu	Pro	Val	Ser
					50				55					60
Met	Gln	Gln	Ile	Tyr	Ser	Asn	Leu	Lys	Tyr	Asn	Val	Ser	Val	Leu
					65				70					75
Asn	Thr	Lys	Ser	Asn	Arg	Thr	Trp	Ser	Gln	Cys	Val	Thr	Asn	His
					80				85					90
Thr	Leu	Val	Leu	Thr	Trp	Leu	Glu	Pro	Asn	Thr	Leu	Tyr	Cys	Val
					95				100					105
His	Val	Glu	Ser	Phe	Val	Pro	Gly	Pro	Pro	Arg	Arg	Ala	Gln	Pro
					110				115					120
Ser	Glu	Lys	Gln	Cys	Ala	Arg	Thr	Leu	Lys	Asp	Gln	Ser	Ser	Glu
					125				130					135
Phe	Lys	Ala	Lys	Ile	Ile	Phe	Trp	Tyr	Val	Leu	Pro	Ile	Ser	Ile
					140				145					150
Thr	Val	Phe	Leu	Phe	Ser	Val	Met	Gly	Tyr	Ser	Ile	Tyr	Arg	Tyr
					155				160					165

Ile His Val Gly Lys Glu Lys His Pro Ala Asn Leu Ile Leu Ile  
 170 175 180  
 Tyr Gly Asn Glu Phe Asp Lys Arg Phe Phe Val Pro Ala Glu Lys  
 185 190 195  
 Ile Val Ile Asn Phe Ile Thr Leu Asn Ile Ser Asp Asp Ser Lys  
 200 205 210  
 Ile Ser His Gln Asp Met Ser Leu Leu Gly Lys Ser Ser Asp Val  
 215 220 225  
 Ser Ser Leu Asn Asp Pro Gln Pro Ser Gly Asn Leu Arg Pro Pro  
 230 235 240  
 Gln Glu Glu Glu Glu Val Lys His Leu Gly Tyr Ala Ser His Leu  
 245 250 255  
 Met Glu Ile Phe Cys Asp Ser Glu Glu Asn Thr Glu Gly Thr Ser  
 260 265 270 ◇  
 Leu Thr Gln Gln Glu Ser Leu Ser Arg Thr Ile Pro Pro Asp Lys  
 275 280 285  
 Thr Val Ile Glu Tyr Glu Tyr Asp Val Arg Thr Thr Asp Ile Cys  
 290 295 300  
 Ala Gly Pro Glu Glu Gln Glu Leu Ser Leu Gln Glu Glu Val Ser  
 305 310 315  
 Thr Gln Gly Thr Leu Leu Glu Ser Gln Ala Ala Leu Ala Val Leu  
 320 325 330  
 Gly Pro Gln Thr Leu Gln Tyr Ser Tyr Thr Pro Gln Leu Gln Asp  
 335 340 345  
 Leu Asp Pro Leu Ala Gln Glu His Thr Asp Ser Glu Glu Gly Pro  
 350 355 360  
 Glu Glu Glu Pro Ser Thr Thr Leu Val Asp Trp Asp Pro Gln Thr  
 365 370 375  
 Gly Arg Leu Cys Ile Pro Ser Leu Ser Ser Phe Asp Gln Asp Ser  
 380 385 390  
 Glu Gly Cys Glu Pro Ser Glu Gly Asp Gly Leu Gly Glu Glu Gly  
 395 400 405  
 Leu Leu Ser Arg Leu Tyr Glu Glu Pro Ala Pro Asp Arg Pro Pro  
 410 415 420  
 Gly Glu Asn Glu Thr Tyr Leu Met Gln Phe Met Glu Glu Trp Gly  
 425 430 435  
 Leu Tyr Val Gln Met Glu Asn  
 440

<210> 105

<211> 21  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-21  
<223> Synthetic construct

<400> 105  
cgctgctgct gttgctcctg g 21

<210> 106  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 106  
cagtgtgcga ggactttg 18

<210> 107  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 107  
agtcgcaggc agcgttgg 18

<210> 108  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 108  
ctccctccgag tctgttgct cctgc 25

<210> 109  
<211> 51  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence

<222> 1-51  
<223> Synthetic construct.

<400> 109  
ggacgggcag ttccctgtgt ctctggtgtt tgccctaaac ctgcaaacat 50

c 51

<210> 110  
<211> 1114  
<212> DNA  
<213> Homo sapiens

<400> 110  
cggacgcgtg ggccggacgcg tggggcgacg cgtgggtctc tgcggggaga 50  
cgccagcctg cgtctgccat ggggctcggg ttgaggggct ggggacgtcc 100  
tctgctgact gtggccaccg ccctgatgct gcccgtgaag ccccccgca 150  
gctcctgggg ggcccagatc atcgggggcc acgaggtgac cccccactcc 200  
aggccctaca tggcatccgt gcgcattcggg ggccaacatc actgcggagg 250  
cttcctgctg cgagcccgct gggtggtctc ggccgcccac tgcttcagcc 300  
acagagacct ccgcactggc ctggtggtgc tgggcgcaca cgtcctgagt 350  
actgcggagc ccacccagca ggtgtttggc atcgatgctc tcaccacgca 400  
ccccgactac cacccatga cccacgcca cgcacatctgc ctgctgcggc 450  
tgaacggctc tgctgtcctg ggccctgcag tggggctgct gaggctgcca 500  
gggagaaggg ccagggcccc cacagcgggg acacggtgcc gggtggtctgg 550  
ctggggcttc gtgtctgact ttgaggagct gccgcctgga ctgatggagg 600  
ccaagggtccg agtgctggac ccggacgtct gcaacagctc ctggaaaggc 650  
cacctgacac ttaccatgct ctgcacccgc agtggggaca gccacagacg 700  
gggcttctgc tcggccgact ccggagggcc cctggtggtgc aggaacctggg 750  
ctcacggcct cgtttccttc tcgggcctct ggtgcggcga ccccaagacc 800  
cccgacgtgt acacgcaggt gtccgcctt gtggcctgga tctggacgt 850  
ggttcggcgg agcagtcccc agcccgcccc cctgcctggg accaccaggc 900  
ccccaggaga agccgcctga gccacaacct tgcggcatgc aaatgagatg 950  
gccgctccag gcctggaatg ttccgtggct gggccccacg ggaagcctga 1000  
tgttcaggggt tggggtgaaa cgggcagcgg tggggcacac ccattccaca 1050  
tgcaaaggc agaagcaaac ccagtaaaat gttaactgac aaaaaaaaaa 1100

aaaaaaaaaa gaaa 1114

<210> 111

<211> 283

<212> PRT

<213> Homo sapiens

<400> 111

Met Gly Leu Gly Leu Arg Gly Trp Gly Arg Pro Leu Leu Thr Val  
1 5 10 15

Ala Thr Ala Leu Met Leu Pro Val Lys Pro Pro Ala Gly Ser Trp  
20 25 30

Gly Ala Gln Ile Ile Gly Gly His Glu Val Thr Pro His Ser Arg  
35 40 45

Pro Tyr Met Ala Ser Val Arg Phe Gly Gly Gln His His Cys Gly  
50 55 60

Gly Phe Leu Leu Arg Ala Arg Trp Val Val Ser Ala Ala His Cys  
65 70 75

Phe Ser His Arg Asp Leu Arg Thr Gly Leu Val Val Leu Gly Ala  
80 85 90

His Val Leu Ser Thr Ala Glu Pro Thr Gln Gln Val Phe Gly Ile  
95 100 105

Asp Ala Leu Thr Thr His Pro Asp Tyr His Pro Met Thr His Ala  
110 115 120

Asn Asp Ile Cys Leu Leu Arg Leu Asn Gly Ser Ala Val Leu Gly  
125 130 135

Pro Ala Val Gly Leu Leu Arg Leu Pro Gly Arg Arg Ala Arg Pro  
140 145 150

Pro Thr Ala Gly Thr Arg Cys Arg Val Ala Gly Trp Gly Phe Val  
155 160 165

Ser Asp Phe Glu Glu Leu Pro Pro Gly Leu Met Glu Ala Lys Val  
170 175 180

Arg Val Leu Asp Pro Asp Val Cys Asn Ser Ser Trp Lys Gly His  
185 190 195

Leu Thr Leu Thr Met Leu Cys Thr Arg Ser Gly Asp Ser His Arg  
200 205 210

Arg Gly Phe Cys Ser Ala Asp Ser Gly Gly Pro Leu Val Cys Arg  
215 220 225

Asn Arg Ala His Gly Leu Val Ser Phe Ser Gly Leu Trp Cys Gly  
230 235 240

Asp Pro Lys Thr Pro Asp Val Tyr Thr Gln Val Ser Ala Phe Val  
245 250 255

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly  
260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala  
275 280

<210> 112  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 112  
gacgtctgca acagctcctg gaag 24

<210> 113  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 113  
cgagaaggaa acgaggccgt gag 23

<210> 114  
<211> 44  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-44  
<223> Synthetic construct.

<400> 114  
tgacacttac catgctctgc acccgcagtg gggacagcca caga 44

<210> 115  
<211> 1808  
<212> DNA  
<213> Homo sapiens

<400> 115  
gagctaccca ggcggctgg gtgcagcaag ctccgcgcgg actccggacg 50  
cctgacgcct gacgcctgtc cccggcccg catgagccgc tacctgctgc 100  
cgctgtcggc gctgggcacg gtagcaggcg ccgccgtgct gctcaaggac 150  
tatgtcaccg gtggggcttg cccccagcaag gccaccatcc ctgggaagac 200

ggtcatcgta acgggcgcca acacaggcat cgggaagcag accgccttgg 250  
aactggccag gagaggaggc aacatcatcc tggcctgccg agacatggag 300  
aagtgtgagg cggcagcaaa ggacatccgc ggggagaccc tcaatcacca 350  
tgtcaacgcc cgccacctgg acttggcttc cctcaagtct atccgagagt 400  
ttgcagcaaa gatcattgaa gaggaggagc gagtgacat tctaataaac 450  
aacgcgggtg ttagtgcggtg cccccactgg accaccgagg acggcttcga 500  
gatgcagttt ggcgttaacc acctgggtca ctttcttgc acaaacttgc 550  
tgctggacaa gctgaaagcc tcagcccctt cgccgatcat caacctctcg 600  
tccctggccc atgttgctgg gcacatagac tttgacgact tgaactggca 650  
gacgaggaag tataacacca aagccgccta ctgccagagc aagctcgcca 700  
tcgtcctctt caccaaggag ctgagccggc ggctgcaagg ctctggtg 750  
actgtcaacg ccctgcaccc cggcgtggcc aggacagagc tggcagaca 800  
cacgggcata catggctcca ctttctccag caccacactc gggcccatct 850  
tctggctgtc ggtcaagagc cccgagctgg ccccccagcc cagcacatac 900  
ctggccgtgg cggaggaact ggccgatgtt tccggaaagt acttcgatgg 950  
actcaaacag aaggccccgg ccccgaggc tgaggatgag gaggtggccc 1000  
ggaggctttg ggctgaaagt gcccgcctgg tgggcttaga ggctccctct 1050  
gtgagggagc agccccctccc cagataacct ctggagcaga tttgaaagcc 1100  
agatggcgc ctccagaccg aggacagctg tccgcacatgc ccgcagcttc 1150  
ctggcactac ctgagccggg agacccagga ctggccggccg ccatgcccgc 1200  
ataggttct agggggcggt gctggccgca gtggactggc ctgcagggtga 1250  
gcactgcccc gggctctggc tggccgtc tgctctgtc ccagcagggg 1300  
agaggggcca tctgatgctt cccctggaa tctaaactgg gaatggccga 1350  
ggaggaaggg gctctgtgca cttgcaggcc acgtcaggag agccagcgg 1400  
gcctgtcggtt gagggttcca aggtgctccg tgaagagcat gggcaagttg 1450  
tctgacactt ggtggattct tgggtccctg tggaccccttgc tgcatgcatt 1500  
gtcctctctg agccttgggtt tcttcagcag tgagatgctc agaataactg 1550  
ctgtctccca ttagtgggtgtg gtacagcggag ctgttgcgt gctatggcat 1600  
ggctgtgccg ggggtgttttgc tgagggttgc cctgtgccag agcccagcca 1650

gagagcagg t gcagggtgtca tccccgagttc aggctctgca cggcatggag 1700  
 tgggaacccc accagactgct gctacaggac ctgggattgc ctgggactcc 1750  
 caccttccta tcaattctca tggtagtcca aactgcagac tctcaaactt 1800  
 gctcattt 1808  
  
 <210> 116  
 <211> 331  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 116  
 Met Ser Arg Tyr Leu Leu Pro Leu Ser Ala Leu Gly Thr Val Ala  
     1              5                 10                 15  
  
 Gly Ala Ala Val Leu Leu Lys Asp Tyr Val Thr Gly Gly Ala Cys  
     20              25                                 30  
  
 Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly  
     35              40                                 45  
  
 Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg  
     50              55                                 60  
  
 Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys  
     65              70                                 75  
  
 Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His  
     80              85                                 90  
  
 Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg  
     95              100                                105  
  
 Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile  
    110              115                                120  
  
 Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr  
    125              130                                135  
  
 Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His  
    140              145                                150  
  
 Phe Leu Leu Thr Asn Leu Leu Asp Lys Leu Lys Ala Ser Ala  
    155              160                                165  
  
 Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly  
    170              175                                180  
  
 His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn  
    185              190                                195  
  
 Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe  
    200              205                                210  
  
 Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val  
    215              220                                225

Asn Ala Leu His Pro Gly Val Ala Arg Thr Glu Leu Gly Arg His  
230 235 240  
Thr Gly Ile His Gly Ser Thr Phe Ser Ser Thr Thr Leu Gly Pro  
245 250 255  
Ile Phe Trp Leu Leu Val Lys Ser Pro Glu Leu Ala Ala Gln Pro  
260 265 270  
Ser Thr Tyr Leu Ala Val Ala Glu Glu Leu Ala Asp Val Ser Gly  
275 280 285  
Lys Tyr Phe Asp Gly Leu Lys Gln Lys Ala Pro Ala Pro Glu Ala  
290 295 300  
Glu Asp Glu Glu Val Ala Arg Arg Leu Trp Ala Glu Ser Ala Arg  
305 310 315  
Leu Val Gly Leu Glu Ala Pro Ser Val Arg Glu Gln Pro Leu Pro  
320 325 330  
Arg

<210> 117  
<211> 2249  
<212> DNA  
<213> Homo sapiens

<400> 117  
gaagttcgcg agcgctggca tgtggtcctg gggcgcggct ggcggcgctg 50  
ctggcggtgc tggcgctcgg gacaggagac ccagaaaggg ctgcggctcg 100  
gggcgacacg ttctcggcgc tgaccagcgt ggcgcgcgcc ctggcgcccg 150  
agcgcggct gctggggctg ctgaggcggt acctgcgcgg ggaggaggcg 200  
cggtcgcccc acctgacttag attctacgac aaggtaactt ctttgcatga 250  
ggattcaaca acccctgtgg ctaaccctct gcttgcattt actctcatca 300  
aacgcctgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350  
gagaacatcc gagctctgaa ggtggctat gagaaggtgg agcaagacct 400  
tccagccttt gaggaccttg agggagcagc aaggcccctg atgcggctgc 450  
aggacgtgta catgctcaat gtgaaaggcc tggcccgagg tgtctttcag 500  
agagtcaactg gctctgccat cactgacctg tacagcccc aacggctctt 550  
ttctctcaca gggatgact gcttccaagt tggcaagggtg gccttatgaca 600  
tgggggatta ttaccatgcc attccatggc tggaggaggc tgtcagtctc 650  
ttccgaggat cttacggaga gtggaagaca gaggatgagg caagtctaga 700

agatgccttg gatcacttgg cctttgctta tttccggca ggaaatgttt 750  
cgtgtccct cagcctctct cgggagtttc ttctctacag cccagataat 800  
aagaggatgg ccaggaatgt cttgaaatat gaaaggctct tggcagagag 850  
cccccaaccac gtggtagctg aggctgtcat ccagaggccc aatatacccc 900  
acctgcagac cagagacacc tacgaggggc tatgtcagac cctgggttcc 950  
cagccccactc tctaccagat ccctagcctc tactgttcct atgagaccaa 1000  
ttccaacgccc tacctgctgc tccagccat ccggaaggag gtcatccacc 1050  
tggagcccta cattgctctc taccatgact tcgtcagtga ctcagaggct 1100  
cagaaaatta gagaacttgc agaaccatgg ctacagaggt cagtgggtgc 1150  
atcaggggag aagcagttac aagtggagta ccgcattcagc aaaagtgcct 1200  
ggctgaagga cactgttgc acaaaactgg tgaccctcaa ccaccgcatt 1250  
gctgccctca caggccttga tgtccggct ccctatgcag agtatctgca 1300  
ggtgtgaac tatggcatcg gaggacacta tgagcctcac tttgaccatg 1350  
ctacgtcacc aagcagcccc ctctacagaa tgaagtcagg aaaccgagtt 1400  
gcaacattta tgatctatct gagctcggtg gaagctggag gagccacagc 1450  
cttcatctat gccaacctca gcgtgcctgt ggttaggaat gcagcactgt 1500  
tttgtggaa cctgcacagg agtgtgaag gggacagtga cacacttcat 1550  
gctggctgtc ctgtcctggt gggagataag tgggtggcca acaagtggat 1600  
acatgagttt ggacaggaat tccgcagacc ctgcagctcc agccctgaag 1650  
actgaactgt tggcagagag aagctgggtgg agtcctgtgg ctttccagag 1700  
aagccaggag ccaaaagctg gggtaggaga ggagaaagca gagcagcctc 1750  
ctggaagaag gccttgcag ctttgtctgt gcctcgcaaa tcagaggcaa 1800  
gggagaggtt gttaccagg gacactgaga atgtacattt gatctgcccc 1850  
agccacggaa gtcagagtag gatgcacagt acaaaggagg gggagtgga 1900  
ggcctgagag ggaagttct ggagttcaga tactctctgt tggAACAGG 1950  
acatctcaac agtctcaggt tcgatcagtg ggtctttgg cactttgaac 2000  
cttgaccaca gggaccaaga agtggcaatg aggacacctg caggaggggc 2050  
tagcctgact cccagaactt taagacttgc tccccactgc cttctgctgc 2100  
agcccaagca gggagtgcc ccctcccaga agcataccc agatgagtgg 2150

tacattatac aaggatTTT ttaagttga aaacaacttt ctttcttt 2200  
 tgtatgatgg ttTTtaaca cagtcatTA aatgtttat aaatcaaaa 2249  
 <210> 118  
 <211> 544  
 <212> PRT  
 <213> Homo sapiens  
 <400> 118  
 Met Gly Pro Gly Ala Arg Leu Ala Ala Leu Leu Ala Val Leu Ala  
 1 5 10 15  
 Leu Gly Thr Gly Asp Pro Glu Arg Ala Ala Ala Arg Gly Asp Thr  
 20 25 30  
 Phe Ser Ala Leu Thr Ser Val Ala Arg Ala Leu Ala Pro Glu Arg  
 35 40 45  
 Arg Leu Leu Gly Leu Leu Arg Arg Tyr Leu Arg Gly Glu Glu Ala  
 50 55 60  
 Arg Leu Arg Asp Leu Thr Arg Phe Tyr Asp Lys Val Leu Ser Leu  
 65 70 75  
 His Glu Asp Ser Thr Thr Pro Val Ala Asn Pro Leu Leu Ala Phe  
 80 85 90  
 Thr Leu Ile Lys Arg Leu Gln Ser Asp Trp Arg Asn Val Val His  
 95 100 105  
 Ser Leu Glu Ala Ser Glu Asn Ile Arg Ala Leu Lys Asp Gly Tyr  
 110 115 120  
 Glu Lys Val Glu Gln Asp Leu Pro Ala Phe Glu Asp Leu Glu Gly  
 125 130 135  
 Ala Ala Arg Ala Leu Met Arg Leu Gln Asp Val Tyr Met Leu Asn  
 140 145 150  
 Val Lys Gly Leu Ala Arg Gly Val Phe Gln Arg Val Thr Gly Ser  
 155 160 165  
 Ala Ile Thr Asp Leu Tyr Ser Pro Lys Arg Leu Phe Ser Leu Thr  
 170 175 180  
 Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly  
 185 190 195  
 Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu  
 200 205 210  
 Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser  
 215 220 225  
 Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala  
 230 235 240

Gly Asn Val Ser Cys Ala Leu Ser Leu Ser Arg Glu Phe Leu Leu  
 245 250 255  
 Tyr Ser Pro Asp Asn Lys Arg Met Ala Arg Asn Val Leu Lys Tyr  
 260 265 270  
 Glu Arg Leu Leu Ala Glu Ser Pro Asn His Val Val Ala Glu Ala  
 275 280 285  
 Val Ile Gln Arg Pro Asn Ile Pro His Leu Gln Thr Arg Asp Thr  
 290 295 300  
 Tyr Glu Gly Leu Cys Gln Thr Leu Gly Ser Gln Pro Thr Leu Tyr  
 305 310 315  
 Gln Ile Pro Ser Leu Tyr Cys Ser Tyr Glu Thr Asn Ser Asn Ala  
 320 325 330  
 Tyr Leu Leu Leu Gln Pro Ile Arg Lys Glu Val Ile His Leu Glu  
 335 340 345  
 Pro Tyr Ile Ala Leu Tyr His Asp Phe Val Ser Asp Ser Glu Ala  
 350 355 360  
 Gln Lys Ile Arg Glu Leu Ala Glu Pro Trp Leu Gln Arg Ser Val  
 365 370 375  
 Val Ala Ser Gly Glu Lys Gln Leu Gln Val Glu Tyr Arg Ile Ser  
 380 385 390  
 Lys Ser Ala Trp Leu Lys Asp Thr Val Asp Pro Lys Leu Val Thr  
 395 400 405  
 Leu Asn His Arg Ile Ala Ala Leu Thr Gly Leu Asp Val Arg Pro  
 410 415 420  
 Pro Tyr Ala Glu Tyr Leu Gln Val Val Asn Tyr Gly Ile Gly Gly  
 425 430 435  
 His Tyr Glu Pro His Phe Asp His Ala Thr Ser Pro Ser Ser Pro  
 440 445 450  
 Leu Tyr Arg Met Lys Ser Gly Asn Arg Val Ala Thr Phe Met Ile  
 455 460 465  
 Tyr Leu Ser Ser Val Glu Ala Gly Gly Ala Thr Ala Phe Ile Tyr  
 470 475 480  
 Ala Asn Leu Ser Val Pro Val Val Arg Asn Ala Ala Leu Phe Trp  
 485 490 495  
 Trp Asn Leu His Arg Ser Gly Glu Gly Asp Ser Asp Thr Leu His  
 500 505 510  
 Ala Gly Cys Pro Val Leu Val Gly Asp Lys Trp Val Ala Asn Lys  
 515 520 525  
 Trp Ile His Glu Tyr Gly Gln Glu Phe Arg Arg Pro Cys Ser Ser



cgccccggact cggagcagg gcgcgtactgc gcgcgcttct cctacacctg 250  
gctcaagttt tcacttatca tctattccac cgtgttctgg ctgattgggg 300  
ccctggtcct gtctgtggc atctatgcag aggttgagcg gcagaaatat 350  
aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcatcctcct 400  
gggcgtcgtc atgttcatgg tctccttcat tggtgtgctg gcgtccctcc 450  
gtgacaacct gtaccttctc caagcattca tgtacatcct tggatctgc 500  
ctcatcatgg agctcattgg tggcgtggg gccttgacct tccggAACCA 550  
gaccattgac ttccctgaacg acaacattcg aagaggaatt gagaactact 600  
atgatgatct ggacttcaaa aacatcatgg actttgttca gaaaaagttc 650  
aagtgtgtg gcggggagga ctaccgagat tggagcaaga atcagtagcca 700  
cgactgcagt gcccctggac ccctggcctg tgggtgccc tacacctgct 750  
gcatcaggaa cacgacagaa gttgtcaaca ccatgtgtgg ctacaaaact 800  
atcgacaagg agcgtttcag tgtgcaggat gtcatctacg tgccgggctg 850  
caccaacgccc gtgatcatct gttcatgga caactacacc atcatggcgt 900  
gcatcctcct gggcatcctg cttccccagt tcctgggggt gctgctgacg 950  
ctgctgtaca tcaccgggt ggaggacatc atcatggagc actctgtcac 1000  
tgatgggctc ctggggcccg gtgccaagcc cagcgtggag gcggcaggca 1050  
cgggatgctg cttgtgctac cccaaattagg gcccagcctg ccatggcagc 1100  
tccaacaagg accgtctggg atagcacctc tcagtcaaca tcgtggggct 1150  
ggacagggct gcggccccc tgcacact cagtaactgac caaagccagg 1200  
gctgtgtgtg cctgtgtgta ggtcccacgg cctctgcctc cccagggagc 1250  
agagcctggg cctccctaa gaggcttcc ccgaggcagc tctggaatct 1300  
gtgcccacct ggggcctggg gaacaaggcc ctcccttctc caggcctggg 1350  
ctacagggga gggagagcct gaggctctgc tcagggccca tttcatctct 1400  
ggcagtgccct tggcgggtt attcaaggca gttttgttagc acctgttaatt 1450  
ggggagaggg agtgtgcccc tcggggcagg agggaaaggc atctggggaa 1500  
ggcaggagg gaagagctgt ccatgcagcc acgccccatgg ccaggttggc 1550  
ctttctcag cctccctagg gccttgagcc ctcttgcaag ggcggctgct 1600  
tccttgagcc tagttttttt ttacgtgatt tttgtaacat tcattttttt 1650

gtacagataa caggagtttc tgactaatca aagctggtat ttcccccgc 1700  
 gtcttattct tgcccttccc ccaaccagt tgttaatcaa acaataaaaa 1750  
 catgttttgt tttgtttta aaaaaaaaa 1778

<210> 123  
 <211> 294  
 <212> PRT  
 <213> Homo sapiens

<400> 123  
 Met Pro Arg Gly Asp Ser Glu Gln Val Arg Tyr Cys Ala Arg Phe  
 1 5 10 15

Ser	Tyr	Leu	Trp	Leu	Lys	Phe	Ser	Leu	Ile	Ile	Tyr	Ser	Thr	Val
20							25							30

Phe	Trp	Leu	Ile	Gly	Ala	Leu	Val	Leu	Ser	Val	Gly	Ile	Tyr	Ala
35									40					45

Glu	Val	Glu	Arg	Gln	Lys	Tyr	Lys	Thr	Leu	Glu	Ser	Ala	Phe	Leu
50									55					60

Ala	Pro	Ala	Ile	Ile	Leu	Ile	Leu	Leu	Gly	Val	Val	Met	Phe	Met
65									70					75

Val	Ser	Phe	Ile	Gly	Val	Leu	Ala	Ser	Leu	Arg	Asp	Asn	Leu	Tyr
80									85					90

Leu	Leu	Gln	Ala	Phe	Met	Tyr	Ile	Leu	Gly	Ile	Cys	Leu	Ile	Met
95									100					105

Glu	Leu	Ile	Gly	Gly	Val	Val	Ala	Leu	Thr	Phe	Arg	Asn	Gln	Thr
110									115					120

Ile	Asp	Phe	Leu	Asn	Asp	Asn	Ile	Arg	Arg	Gly	Ile	Glu	Asn	Tyr
125									130					135

Tyr	Asp	Asp	Leu	Asp	Phe	Lys	Asn	Ile	Met	Asp	Phe	Val	Gln	Lys
140									145					150

Lys	Phe	Lys	Cys	Cys	Gly	Gly	Glu	Asp	Tyr	Arg	Asp	Trp	Ser	Lys
155									160					165

Asn	Gln	Tyr	His	Asp	Cys	Ser	Ala	Pro	Gly	Pro	Leu	Ala	Cys	Gly
170									175					180

Val	Pro	Tyr	Thr	Cys	Cys	Ile	Arg	Asn	Thr	Thr	Glu	Val	Val	Asn
185									190					195

Thr	Met	Cys	Gly	Tyr	Lys	Thr	Ile	Asp	Lys	Glu	Arg	Phe	Ser	Val
200									205					210

Gln	Asp	Val	Ile	Tyr	Val	Arg	Gly	Cys	Thr	Asn	Ala	Val	Ile	Ile
215									220					225

Trp	Phe	Met	Asp	Asn	Tyr	Thr	Ile	Met	Ala	Cys	Ile	Leu	Leu	Gly

230	235	240
Ile Leu Leu Pro Gln Phe Leu Gly Val	Leu Leu Thr Leu Leu Tyr	
245	250	255
Ile Thr Arg Val Glu Asp Ile Ile Met	Glu His Ser Val Thr Asp	
260	265	270
Gly Leu Leu Gly Pro Gly Ala Lys Pro	Ser Val Glu Ala Ala Gly	
275	280	285
Thr Gly Cys Cys Leu Cys Tyr Pro Asn		
290		

<210> 124  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 124  
atcatctatt ccaccgtgtt ctggc 25

<210> 125  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 125  
gacagagtgc tccatgatga tgtcc 25

<210> 126  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 126  
cctgtctgtg ggcatctatg cagaggttga gcggcagaaa tataaaaccc 50

<210> 127  
<211> 1636  
<212> DNA  
<213> Homo sapiens

<400> 127  
gaggagcggg ccgaggactc cagcgtgccccc aggtctggca tcctgcactt 50  
gctgccctct gacacctggg aagatggccg gcccgtggac cttcaccctt 100  
ctctgtggtt tgctggcagc caccttgatc caagccaccc tcagtcccac 150  
tgcatgttc atcctcgcc caaaagtcat caaagaaaag ctgacacagg 200  
agctgaagga ccacaacgcc accagcatcc tgcatcagct gcccgtgctc 250  
agtgcacatgc gggaaaagcc agccggaggc atccctgtgc tggcagccct 300  
ggtgaacacc gtcctgaagc acatcatctg gctgaaggc atcacagcta 350  
acatccctcca gctgcaggtg aagccctcg acaatgacca ggagctgcta 400  
gtcaagatcc ccctggacat ggtggctgga ttcaacacgc ccctggtaa 450  
gaccatcgtg gagttccaca tgacgactga ggcccaagcc accatccgca 500  
tggacaccag tgcaagtggc cccacccggc tggctcttag tgactgtgcc 550  
accagccatg ggagcctgctg catccaaactg ctgtataaagc ttccttcct 600  
ggtgaacgc tttagctaagc aggtcatgaa cctccttagtg ccattccctgc 650  
ccaatcttagt gaaaaaccag ctgtgtcccg tgatcgaggc ttccctcaat 700  
ggcatgtatg cagacccct gcagctggtg aaggtgcca ttccctcag 750  
cattgaccgt ctggagtttgc accttctgtt tcctgccatc aagggtgaca 800  
ccattcagct ctacctgggg gccaagttgt tggactcaca gggaaagggtg 850  
accaagtggt tcaataactc tgcatcgttcc ctgacaatgc ccaccctgga 900  
caacatcccg ttcatcgttca tcgtgagtca ggacgtggtg aaagctgcag 950  
tggtctgtgt gctctctcca gaagaattca tggctctgtt ggactctgtg 1000  
cttcctgaga gtgccccatcg gctgaagtca agcatcgggc tgatcaatga 1050  
aaaggctgca gataagctgg gatctaccga gatcgtgaag atcctaactc 1100  
aggacactcc cgagttttt atagaccaag gccatgcca ggtggcccaa 1150  
ctgatcgtgc tggaaagtgtt tccctccagt gaagccctcc gccccttgg 1200  
caccctgggc atcgaagcca gctcggaaagc tcagtttac accaaagggtg 1250  
accaacttat actcaacttg aataacatca gctctgtatcg gatccagctg 1300  
atgaactctg ggattggctg gttccaaacct gatgttctga aaaacatcat 1350  
cactgagatc atccacttcca tcctgctgcc gaaccagaat gcacaaattaa 1400  
gatctgggggt cccagtgta ttggtaagg cttgggatt cgaggcagct 1450

gagtcctcac tgaccaagga tgcccttgcg cttactccag ccccttgcg 1500  
 gaaaccaggc tccctgtct cccagtgaag acttggatgg cagccatcg 1550  
 ggaaggctgg gtcccagctg ggagtatgg tgtgagctct atagaccatc 1600  
 cctctctgca atcaataaac acttgccctgt gaaaaa 1636

<210> 128  
 <211> 484  
 <212> PRT  
 <213> Homo sapiens

<400> 128

Met	Ala	Gly	Pro	Trp	Thr	Phe	Thr	Leu	Leu	Cys	Gly	Leu	Leu	Ala
1				5				10						15

Ala	Thr	Leu	Ile	Gln	Ala	Thr	Leu	Ser	Pro	Thr	Ala	Val	Leu	Ile
				20				25						30

Leu	Gly	Pro	Lys	Val	Ile	Lys	Glu	Lys	Leu	Thr	Gln	Glu	Leu	Lys
				35				40						45

Asp	His	Asn	Ala	Thr	Ser	Ile	Leu	Gln	Gln	Leu	Pro	Leu	Leu	Ser
				50				55						60

Ala	Met	Arg	Glu	Lys	Pro	Ala	Gly	Gly	Ile	Pro	Val	Leu	Gly	Ser
				65				70						75

Leu	Val	Asn	Thr	Val	Leu	Lys	His	Ile	Ile	Trp	Leu	Lys	Val	Ile
				80				85						90

Thr	Ala	Asn	Ile	Leu	Gln	Leu	Gln	Val	Lys	Pro	Ser	Ala	Asn	Asp
				95				100						105

Gln	Glu	Leu	Leu	Val	Lys	Ile	Pro	Leu	Asp	Met	Val	Ala	Gly	Phe
				110				115						120

Asn	Thr	Pro	Leu	Val	Lys	Thr	Ile	Val	Glu	Phe	His	Met	Thr	Thr
				125				130						135

Glu	Ala	Gln	Ala	Thr	Ile	Arg	Met	Asp	Thr	Ser	Ala	Ser	Gly	Pro
				140				145						150

Thr	Arg	Leu	Val	Leu	Ser	Asp	Cys	Ala	Thr	Ser	His	Gly	Ser	Leu
				155				160						165

Arg	Ile	Gln	Leu	Leu	Tyr	Lys	Leu	Ser	Phe	Leu	Val	Asn	Ala	Leu
				170				175						180

Ala	Lys	Gln	Val	Met	Asn	Leu	Leu	Val	Pro	Ser	Leu	Pro	Asn	Leu
				185				190						195

Val	Lys	Asn	Gln	Leu	Cys	Pro	Val	Ile	Glu	Ala	Ser	Phe	Asn	Gly
				200				205						210

Met	Tyr	Ala	Asp	Leu	Leu	Gln	Leu	Val	Lys	Val	Pro	Ile	Ser	Leu
				215				220						225

Ser Ile Asp Arg Leu Glu Phe Asp Leu Leu Tyr Pro Ala Ile Lys  
 230 235 240  
 Gly Asp Thr Ile Gln Leu Tyr Leu Gly Ala Lys Leu Leu Asp Ser  
 245 250 255  
 Gln Gly Lys Val Thr Lys Trp Phe Asn Asn Ser Ala Ala Ser Leu  
 260 265 270  
 Thr Met Pro Thr Leu Asp Asn Ile Pro Phe Ser Leu Ile Val Ser  
 275 280 285  
 Gln Asp Val Val Lys Ala Ala Val Ala Val Leu Ser Pro Glu  
 290 295 300  
 Glu Phe Met Val Leu Leu Asp Ser Val Leu Pro Glu Ser Ala His  
 305 310 315  
 Arg Leu Lys Ser Ser Ile Gly Leu Ile Asn Glu Lys Ala Ala Asp  
 320 325 330  
 Lys Leu Gly Ser Thr Gln Ile Val Lys Ile Leu Thr Gln Asp Thr  
 335 340 345  
 Pro Glu Phe Phe Ile Asp Gln Gly His Ala Lys Val Ala Gln Leu  
 350 355 360  
 Ile Val Leu Glu Val Phe Pro Ser Ser Glu Ala Leu Arg Pro Leu  
 365 370 375  
 Phe Thr Leu Gly Ile Glu Ala Ser Ser Glu Ala Gln Phe Tyr Thr  
 380 385 390  
 Lys Gly Asp Gln Leu Ile Leu Asn Leu Asn Asn Ile Ser Ser Asp  
 395 400 405  
 Arg Ile Gln Leu Met Asn Ser Gly Ile Gly Trp Phe Gln Pro Asp  
 410 415 420  
 Val Leu Lys Asn Ile Ile Thr Glu Ile Ile His Ser Ile Leu Leu  
 425 430 435  
 Pro Asn Gln Asn Gly Lys Leu Arg Ser Gly Val Pro Val Ser Leu  
 440 445 450  
 Val Lys Ala Leu Gly Phe Glu Ala Ala Glu Ser Ser Leu Thr Lys  
 455 460 465  
 Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser  
 470 475 480  
 Pro Val Ser Gln

<210> 129  
 <211> 2213  
 <212> DNA  
 <213> Homo sapiens

<400> 129  
gagcgaacat ggcagcgcgt tggcggtttt ggtgtgtctc tgtgaccatg 50  
gtggggcgc tgctcatcgt ttgcgacgtt ccctcagcct ctgccccaaag 100  
aaagaaggag atgggttat ctgaaaaggt tagtcagctg atggaatgga 150  
ctaacaaaag acctgtaata agaatgaatg gagacaagtt ccgtcgccct 200  
gtgaaagccc caccgagaaa ttactccgtt atcgtcatgt tcactgctct 250  
ccaaactgcat agacagtgtg tcgtttgcaa gcaagctgat gaagaattcc 300  
agatcctggc aaactcctgg cgatactcca gtgcattcac caacaggata 350  
tttttgcca tggtgattt tcatgaaggc tctgatgtat ttcatgatgct 400  
aaacatgaat tcagctccaa ctttcatcaa ctttcctgca aaaggaaac 450  
ccaaacgggg tgatacatat gagttacagg tgcggggttt ttcatgatgag 500  
cagattgccc ggtggatcgc cgacagaact gatgtcaata ttagagtgtat 550  
tagaccccca aattatgctg gtccccttat gttgggattt ctttggctg 600  
ttattggtg acttgtgtat ctgcgaagaa gtaatatgga atttctctt 650  
aataaaaactg gatgggcttt tgcagcttg tgtttgc tgcataatgac 700  
atctggtcaa atgtgaaacc atataagagg accaccatat gcccataaga 750  
atccccacac gggacatgtg aattatatcc atggaagcag tcaagcccag 800  
ttttagctg aaacacacat ttttcttctg ttatggtg gagttacatt 850  
aggaatggtg ctttatgtg aagctgctac ctctgacatg gatattggaa 900  
agcgaaagat aatgtgtgtg gctggattt gacttgtgtt attattcttc 950  
agttggatgc tctctatattt tagatctaaa tatcatggct acccatacag 1000  
ctttctgatg agtaaaaag gtcccagaga tatatagaca ctggagtact 1050  
ggaaattgaa aaacgaaaat cgtgtgtgt tgaaaagaag aatgcaactt 1100  
gtatattttg tattacctct tttttcaag tgatttaat agttaatcat 1150  
ttaaccaaag aagatgtgt agtccttaac aagcaatcct ctgtcaaaat 1200  
ctgaggtatt tgaaaataat tatcctctt accttctctt cccagtgaac 1250  
tttatggAAC attaatttA gtacaattAA gtatatttATA aaaattgtAA 1300  
aactactact ttgttttagt tagaacaAAAG ctcaaaACTA cttagttaA 1350  
cttggtcATC tgatTTATA ttgccttATC caaAGATGGG gaaAGTAAGT 1400  
cctgaccagg tgTTCCcaca tatgcctgtt acagataact acattaggaa 1450

ttcattctta gcttcttcat ctttgtgtgg atgtgtatac tttacgcata 1500  
tttccttttg agtagagaaa ttatgtgtgt catgtggctc tctgaaaatg 1550  
gaacaccatt cttagagca cacgtctagc cctcagcaag acagttgttt 1600  
ctccctcctcc ttgcataattt cctactgcgc tccagcctga gtgatagagt 1650  
gagactctgt ctcaaaaaaa agtatctcta aatacaggat tataatttct 1700  
gcttgagttat ggtgttaact accttgtatt tagaaagatt tcagattcat 1750  
tccatctcct tagtttctt ttaaggtgac ccatctgtga taaaaatata 1800  
gcttagtgct aaaatcagtg taacttatac atggcctaaa atgtttctac 1850  
aaatttagagt ttgtcactta ttccatttgtt acctaagaga aaaataggct 1900  
cagttagaaa aggactccct gcccaggcgc agtgaattac gcctgtaatc 1950  
tcagcacttt gggaggccaa ggcaggcaga tcacgaggc aggagttcga 2000  
gaccatcctg gccaacatgg tgaaaccccg tctctactaa aaatataaaa 2050  
attagctggg tgtggtggca ggagcctgta atcccagcta cacaggaggc 2100  
tgaggcacga gaatcacttg aactcaggag atggaggttt cagtgagccg 2150  
agatcacgccc actgcactcc agcctggcaa cagagcgaga ctccatctca 2200  
aaaaaaaaaa aaa 2213

<210> 130  
<211> 335  
<212> PRT  
<213> Homo sapiens

<400> 130  
Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val  
1 5 10 15  
Val Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln  
20 25 30  
Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met  
35 40 45  
Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys  
50 55 60  
Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile  
65 70 75  
Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys  
80 85 90  
Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg  
95 100 105

Tyr Ser Ser Ala Phe Thr Asn Arg Ile Phe Phe Ala Met Val Asp  
 110 115 120  
 Phe Asp Glu Gly Ser Asp Val Phe Gln Met Leu Asn Met Asn Ser  
 125 130 135  
 Ala Pro Thr Phe Ile Asn Phe Pro Ala Lys Gly Lys Pro Lys Arg  
 140 145 150  
 Gly Asp Thr Tyr Glu Leu Gln Val Arg Gly Phe Ser Ala Glu Gln  
 155 160 165  
 Ile Ala Arg Trp Ile Ala Asp Arg Thr Asp Val Asn Ile Arg Val  
 170 175 180  
 Ile Arg Pro Pro Asn Tyr Ala Gly Pro Leu Met Leu Gly Leu Leu  
 185 190 195  
 Leu Ala Val Ile Gly Gly Leu Val Tyr Leu Arg Arg Ser Asn Met  
 200 205 210  
 Glu Phe Leu Phe Asn Lys Thr Gly Trp Ala Phe Ala Ala Leu Cys  
 215 220 225  
 Phe Val Leu Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg  
 230 235 240  
 Gly Pro Pro Tyr Ala His Lys Asn Pro His Thr Gly His Val Asn  
 245 250 255  
 Tyr Ile His Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Thr His  
 260 265 270  
 Ile Val Leu Leu Phe Asn Gly Gly Val Thr Leu Gly Met Val Leu  
 275 280 285  
 Leu Cys Glu Ala Ala Thr Ser Asp Met Asp Ile Gly Lys Arg Lys  
 290 295 300  
 Ile Met Cys Val Ala Gly Ile Gly Leu Val Val Leu Phe Phe Ser  
 305 310 315  
 Trp Met Leu Ser Ile Phe Arg Ser Lys Tyr His Gly Tyr Pro Tyr  
 320 325 330  
 Ser Phe Leu Met Ser  
 335

<210> 131  
 <211> 2476  
 <212> DNA  
 <213> Homo sapiens

<400> 131  
 aagcaaccaa actgcaagct ttgggagttt ttcgcgtgtcc ctgccctgct 50  
 ctgcttaggaa gagaacgcca gagggaggcg gctggcccg cggcaggctc 100

tcagaaccgc taccggcgat gctactgctg tgggtgtcgg tggtcgcagc 150  
cttggcgctg gcggtaactgg ccccccggagc aggggagcag aggcggagag 200  
cagccaaagc gcccaatgtg gtgctggtcg tgagcgactc ctgcgtatgga 250  
aggtaacat ttcatccagg aagtcaggta gtgaaacttc cttttatcaa 300  
ctttatgaag acacgtggga ctccctttct gaatgcctac acaaactctc 350  
caatttggtg cccatcacgc gcagcaatgt ggagtggcct ctgcactcac 400  
ttaacagaat ctggaataa ttttaggggt ctagatccaa attatacaac 450  
atggatggat gtcatggaga ggcatggcta ccgaacacag aaatttggga 500  
aactggacta tacttcagga catcactcca ttagtaatcg tgtgaaagcg 550  
tggacaagag atgttgctt ctactcaga caagaaggca ggcccatgg 600  
taatcttatac cgtaacagga ctaaagttag agttagggaa agggattggc 650  
agaatacaga caaaggcagta aactggtaa gaaaggaagc aattaattac 700  
actgaaccat ttgttattta ctgggatta aatttaccac acccttaccc 750  
ttcaccatct tctggagaaa attttggatc ttcaacattt cacacatctc 800  
tttattggct tgaaaaagtg tctcatgatg ccatcaaaat cccaaagtgg 850  
tcaccttgt cagaaatgca ccctgttagat tattactctt ctatataaaa 900  
aaactgcact ggaagattta caaaaaaaga aattaagaat attagagcat 950  
tttattatgc tatgtgtgct gagacagatg ccatgcttgg tggaaattatt 1000  
ttggcccttc atcaattaga tcttcttcag aaaactattg tcataactc 1050  
ctcagaccat ggagagctgg ccatggaaaca tcgacagttt tataaaatga 1100  
gcatgtacga ggcttagtgca catgttccgc ttttgatgat gggaccagga 1150  
attnaagccg gcctacaagt atcaaatgtg gtttctcttgg tggatattta 1200  
ccctaccatg cttgatatttgc ctggatttcc tctgcctcag aacctgagtg 1250  
gatactctt gttgccgtta tcatcagaaa catttaagaa tgaacataaaa 1300  
gtcaaaaacc tgcattccacc ctggattctg agtgaattcc atggatgtaa 1350  
tgtgaatgcc tccaccatca tgcttcgaac taaccactgg aaatatata 1400  
cctattcggta tggtgcatca atattgcctc aactcttgc tcttcctcg 1450  
gatccagatg aattaacaaa tggtgctgta aaatttccag aaattactta 1500  
ttctttggat cagaagcttc attccattat aaactaccct aaagttctg 1550

cttctgtcca ccagtataat aaagagcagt ttatcaagtg gaaacaaga 1600  
ataggacaga attattcaaa cgttatacgca aatcttaggt ggcaccaaga 1650  
ctggcagaag gaaccaagga agtatgaaaa tgcaattgat cagtggctta 1700  
aaacccatat gaatccaaga gcagttgaa caaaaagttt aaaaatagtg 1750  
ttcttagagat acatataaat atattacaag atcataatta tgtatTTAA 1800  
atgaaacagt tttaataatt accaagttt ggccgggcac agtggctcac 1850  
acctgttaatc ccaggacttt gggaggctga ggaaagcaga tcacaaggc 1900  
aagagattga gaccatcctg gccaacatgg tgaaaccctg tctctactaa 1950  
aaatacaaaa attagctggg cgcgggtggc cacacctata gtctcagcta 2000  
ctcagaggct gaggcaggag gatcgcttga acccgggagg cagcagttgc 2050  
agttagctga gattgcGCCA ctgtactCCA gcctggcaac agagttagac 2100  
tgtgtcgcaa aaaaataaaa ataaaataat aataattacc aatttttcat 2150  
tattttgtaa gaatgttagt tattttaga taaaatGCCA atgattataa 2200  
aatcacatata ttcaaaaat gtttatttt taggccttgc tacaatttct 2250  
aacaatttag tggaaagtatc aaaaggattg aagcaaatac tgtaacagtt 2300  
atgttccttt aaataataga gaatataaaa tattgtata atatgtatca 2350  
taaaatagtt gtatgtgagc atttgatggt gaaaaaaaaaaaaaaa 2400  
aaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 2450  
aaaaaaaaaaa aaaaaaaaaaaa aaaaaaa 2476

<210> 132  
<211> 536  
<212> PRT  
<213> Homo sapiens

<400> 132  
Met Leu Leu Leu Trp Val Ser Val Val Ala Ala Leu Ala Leu Ala  
1 5 10 15  
Val Leu Ala Pro Gly Ala Gly Glu Gln Arg Arg Arg Ala Ala Lys  
20 25 30  
Ala Pro Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg  
35 40 45  
Leu Thr Phe His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile  
50 55 60  
Asn Phe Met Lys Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr  
65 70 75

Asn Ser Pro Ile Cys Cys Pro Ser Arg Ala Ala Met Trp Ser Gly  
                   80                     85                         90

Leu Phe Thr His Leu Thr Glu Ser Trp Asn Asn Phe Lys Gly Leu  
                   95                     100                     105

Asp Pro Asn Tyr Thr Trp Met Asp Val Met Glu Arg His Gly  
                   110                    115                     120

Tyr Arg Thr Gln Lys Phe Gly Lys Leu Asp Tyr Thr Ser Gly His  
                   125                    130                     135

His Ser Ile Ser Asn Arg Val Glu Ala Trp Thr Arg Asp Val Ala  
                   140                    145                     150

Phe Leu Leu Arg Gln Glu Gly Arg Pro Met Val Asn Leu Ile Arg  
                   155                    160                     165

Asn Arg Thr Lys Val Arg Val Met Glu Arg Asp Trp Gln Asn Thr  
                   170                    175                     180

Asp Lys Ala Val Asn Trp Leu Arg Lys Glu Ala Ile Asn Tyr Thr  
                   185                    190                     195

Glu Pro Phe Val Ile Tyr Leu Gly Leu Asn Leu Pro His Pro Tyr  
                   200                    205                     210

Pro Ser Pro Ser Ser Gly Glu Asn Phe Gly Ser Ser Thr Phe His  
                   215                    220                     225

Thr Ser Leu Tyr Trp Leu Glu Lys Val Ser His Asp Ala Ile Lys  
                   230                    235                     240

Ile Pro Lys Trp Ser Pro Leu Ser Glu Met His Pro Val Asp Tyr  
                   245                    250                     255

Tyr Ser Ser Tyr Thr Lys Asn Cys Thr Gly Arg Phe Thr Lys Lys  
                   260                    265                     270

Glu Ile Lys Asn Ile Arg Ala Phe Tyr Tyr Ala Met Cys Ala Glu  
                   275                    280                     285

Thr Asp Ala Met Leu Gly Glu Ile Ile Leu Ala Leu His Gln Leu  
                   290                    295                     300

Asp Leu Leu Gln Lys Thr Ile Val Ile Tyr Ser Ser Asp His Gly  
                   305                    310                     315

Glu Leu Ala Met Glu His Arg Gln Phe Tyr Lys Met Ser Met Tyr  
                   320                    325                     330

Glu Ala Ser Ala His Val Pro Leu Leu Met Met Gly Pro Gly Ile  
                   335                    340                     345

Lys Ala Gly Leu Gln Val Ser Asn Val Val Ser Leu Val Asp Ile  
                   350                    355                     360

Tyr Pro Thr Met Leu Asp Ile Ala Gly Ile Pro Leu Pro Gln Asn

365	370	375
Leu Ser Gly Tyr Ser Leu Leu Pro Leu	Ser Ser Glu Thr Phe Lys	
380	385	390
Asn Glu His Lys Val Lys Asn Leu His	Pro Pro Trp Ile Leu Ser	
395	400	405
Glu Phe His Gly Cys Asn Val Asn Ala	Ser Thr Tyr Met Leu Arg	
410	415	420
Thr Asn His Trp Lys Tyr Ile Ala Tyr	Ser Asp Gly Ala Ser Ile	
425	430	435
Leu Pro Gln Leu Phe Asp Leu Ser Ser	Asp Pro Asp Glu Leu Thr	
440	445	450
Asn Val Ala Val Lys Phe Pro Glu Ile	Thr Tyr Ser Leu Asp Gln	
455	460	465
Lys Leu His Ser Ile Ile Asn Tyr Pro	Lys Val Ser Ala Ser Val	
470	475	480
His Gln Tyr Asn Lys Glu Gln Phe Ile	Lys Trp Lys Gln Ser Ile	
485	490	495
Gly Gln Asn Tyr Ser Asn Val Ile Ala	Asn Leu Arg Trp His Gln	
500	505	510
Asp Trp Gln Lys Glu Pro Arg Lys Tyr	Glu Asn Ala Ile Asp Gln	
515	520	525
Trp Leu Lys Thr His Met Asn Pro Arg Ala Val		
530	535	

<210> 133  
<211> 1475  
<212> DNA  
<213> Homo sapiens

<400> 133  
gagagaagtc agcctggcag agagactctg aatgaggga ttagaggtgt 50  
tcaaggagca agagttcag cctgaagaca agggagcagt ccctgaagac 100  
gcttctactg agaggtctgc catggcctct cttggcctcc aacttgtgg 150  
ctacatccta ggccttctgg ggctttggg cacactggtt gccatgctgc 200  
tccccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250  
gttggcttct ccaaggcct ctggatggaa tgtgccacac acagcacagg 300  
catcacccag tgtgacatct atagcaccct tctggcctg cccgctgaca 350  
tccaggctgc ccaggccatg atggtgacat ccagtgcaat ctcctccctg 400  
gcctgcatta tctctgtggt gggcatgaga tgcacagtct tctgccagga 450

atcccggacc aaagacagag tggcggttagc aggtggagtc ttttcatcc 500  
ttggaggcct cctgggattc attcctgttg cctggaatct tcataggatc 550  
ctacgggact tctactcacc actggtgctt gacagcatga aatttgagat 600  
tggagaggct cttaacttgg gcattatttc ttccctgttc tccctgata 650  
ctggaaatcat cctctgcttt tcctgctcat cccagagaaa tcgctccaac 700  
tactacgatg cctaccaagc ccaacctttt gccacaagga gctctccaag 750  
gcctggtcaa cctccaaag tcaagagtga gttcaattcc tacagcctga 800  
cagggtatgt gtgaagaacc agggggcaga gctgggggtt ggctgggtct 850  
gtaaaaaaca gtggacagca ccccgaggc cacaggtgag ggacactacc 900  
actggatcgt gtcagaaggt gctgctgagg atagactgac tttggccatt 950  
ggattgagca aaggcagaaa tggggctag tgtaacagca tgcaggttga 1000  
attgccaagg atgctcgcca tgccagcctt tctgtttcc tcacccctgt 1050  
gctccccctgc cctaagtccc caaccctcaa cttgaaaccc cattccctta 1100  
agccaggact cagaggatcc ctttgcctc tggtttacctt gggactccat 1150  
ccccaaaccc actaatcaca tcccactgac tgaccctctg tgatcaaaga 1200  
ccctctctct ggctgaggtt ggctcttagc tcattgctgg gnatgggaag 1250  
gagaagcagt ggctttgtg ggcattgctc taacctactt ctcaagcttc 1300  
cctccaaaga aactgattgg ccctggAACc tccatcccac tcttgttatg 1350  
actccacagt gtccagacta atttgtcat gaactgaaat aaaaccatcc 1400  
tacggtatcc agggAACAGA aagcaggatg caggatgggaa gacagggaaag 1450  
gcagcctggg acattaaaaa aaata 1475

<210> 134  
<211> 230  
<212> PRT  
<213> Homo sapiens

<400> 134  
Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu  
1 5 10 15  
Leu Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp  
20 25 30  
Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly  
35 40 45  
Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly

50	55	60
Ile Thr Gln Cys Asp Ile Tyr Ser Thr	Leu Leu Gly Leu Pro Ala	
65	70	75
Asp Ile Gln Ala Ala Gln Ala Met Met Val	Thr Ser Ser Ala Ile	
80	85	90
Ser Ser Leu Ala Cys Ile Ile Ser Val Val	Gly Met Arg Cys Thr	
95	100	105
Val Phe Cys Gln Glu Ser Arg Ala Lys Asp	Arg Val Ala Val Ala	
110	115	120
Gly Gly Val Phe Phe Ile Leu Gly Gly	Leu Leu Gly Phe Ile Pro	
125	130	135
Val Ala Trp Asn Leu His Gly Ile Leu Arg Asp	Phe Tyr Ser Pro	
140	145	150
Leu Val Pro Asp Ser Met Lys Phe Glu Ile	Gly Glu Ala Leu Tyr	
155	160	165
Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu	Ile Ala Gly Ile Ile	
170	175	180
Leu Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg	Ser Asn Tyr Tyr	
185	190	195
Asp Ala Tyr Gln Ala Gln Pro Leu Ala Thr Arg	Ser Ser Pro Arg	
200	205	210
Pro Gly Gln Pro Pro Lys Val Lys Ser Glu	Phe Asn Ser Tyr Ser	
215	220	225
Leu Thr Gly Tyr Val		
230		

<210> 135  
<211> 610  
<212> DNA  
<213> Homo sapiens

<400> 135  
gcactgctgc tgtccatca gctgctctga agctccatgg tgcccagaat 50  
cttcgctcct gcttatgtgt cagtctgtct cctcctcttg tgtccaaggg 100  
aagtcatcgc tcccgctggc tcagaaccat ggctgtgcca gccggcaccc 150  
aggtgtggag acaagatcta caaccccttg gagcagtgct gttacaatga 200  
cgccatcgtg tccctgagcg agacccgcca atgtggccc ccctgcacct 250  
tctggccctg ctttgagctc tgctgtcttg attccttgg cctcacaaac 300  
gattttgttgc tgaagctgaa ggttcaggggt gtgaattccc agtgccactc 350

atctcccatc tccagtaaat gtgaaagcag aagacgtttt ccctgagaag 400  
 acatagaaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450  
 aggttatatg tgtaccagta gagaagcctg aggaatttac aaaatgtgc 500  
 agctccaagc cattgtatgg cccatgtggg agactgtatgg gacatggaga 550  
 atgacagtag attatcagga aataaataaa gtggttttc caatgtacac 600  
 acctgtaaaa 610

<210> 136  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 136

Met	Val	Pro	Arg	Ile	Phe	Ala	Pro	Ala	Tyr	Val	Ser	Val	Cys	Leu
1					5					10			15	

Leu	Leu	Leu	Cys	Pro	Arg	Glu	Val	Ile	Ala	Pro	Ala	Gly	Ser	Glu
						20			25			30		

Pro	Trp	Leu	Cys	Gln	Pro	Ala	Pro	Arg	Cys	Gly	Asp	Lys	Ile	Tyr
					35				40			45		

Asn	Pro	Leu	Glu	Gln	Cys	Cys	Tyr	Asn	Asp	Ala	Ile	Val	Ser	Leu
					50				55			60		

Ser	Glu	Thr	Arg	Gln	Cys	Gly	Pro	Pro	Cys	Thr	Phe	Trp	Pro	Cys
					65				70			75		

Phe	Glu	Leu	Cys	Cys	Leu	Asp	Ser	Phe	Gly	Leu	Thr	Asn	Asp	Phe
					80				85			90		

Val	Val	Lys	Leu	Lys	Val	Gln	Gly	Val	Asn	Ser	Gln	Cys	His	Ser
					95				100			105		

Ser	Pro	Ile	Ser	Ser	Lys	Cys	Glu	Ser	Arg	Arg	Arg	Phe	Pro	
					110				115					

<210> 137  
 <211> 771  
 <212> DNA  
 <213> Homo sapiens

<400> 137

```

  ctccactgca accacccaga gccatggctc cccgaggctg catcgtagct 50
  gtctttgcca ttttctgcat ctccaggctc ctctgctcac acggagcccc 100
  agtggccccc atgactcctt acctgtatgt gtgccagcca cacaagagat 150
  gtggggacaa gttctacgac cccctgcagc actgttgcta tgatgtatgcc 200
  gtcgtgccct tggccaggac ccagacgtgt ggaaactgca ctttcagagt 250
  
```

ctgcttgag cagtgcgtcc cctggacctt catggtaag ctgataaaacc 300  
agaactgcga ctcagccccg acctcgatg acaggcttg tcgcagtgtc 350  
agctaatttgcgaa acatcagggg aacgatgact cctggattct ctttcctggg 400  
tgggccttggaa gaaagaggct ggtgttacct gagatctggg atgctgagt 450  
gctgtttggg ggccagagaa acacacactc aactgcccac ttcattctgt 500  
gacctgtctg aggcccaccc tgcagctgcc ctgaggaggc ccacaggtcc 550  
ccttcttagaa ttctggacag catgagatgc gtgtgctgat gggggcccaag 600  
ggactctgaa ccctcctgat gaccctatg gccaacatca acccggcacc 650  
accccaaggc tggctgggaa acccttcacc cttctgtgag attttccatc 700  
atctcaagtt ctcttctatc caggagcaaa gcacaggatc ataataaaatt 750  
tatgtacttt ataaatgaaa a 771

<210> 138

<211> 110

<212> PRT

<213> Homo sapiens

<400> 138

Met	Ala	Pro	Arg	Gly	Cys	Ile	Val	Ala	Val	Phe	Ala	Ile	Phe	Cys
1				5					10				15	
Ile	Ser	Arg	Leu	Leu	Cys	Ser	His	Gly	Ala	Pro	Val	Ala	Pro	Met
				20				25					30	
Thr	Pro	Tyr	Leu	Met	Leu	Cys	Gln	Pro	His	Lys	Arg	Cys	Gly	Asp
				35				40				45		
Lys	Phe	Tyr	Asp	Pro	Leu	Gln	His	Cys	Cys	Tyr	Asp	Asp	Ala	Val
				50				55				60		
Val	Pro	Leu	Ala	Arg	Thr	Gln	Thr	Cys	Gly	Asn	Cys	Thr	Phe	Arg
				65				70				75		
Val	Cys	Phe	Glu	Gln	Cys	Cys	Pro	Trp	Thr	Phe	Met	Val	Lys	Leu
				.80				85				90		
Ile	Asn	Gln	Asn	Cys	Asp	Ser	Ala	Arg	Thr	Ser	Asp	Asp	Arg	Leu
				95				100				105		
Cys	Arg	Ser	Val	Ser										
				110										

<210> 139

<211> 2044

<212> DNA

<213> Homo sapiens

<400> 139

gggggcgggt gcctggagca cggcgctggg gccggccgca ggcgtcactc 50  
gctcgcactc agtcgcggga ggcttccccg cgccggccgc gtcccgcccc 100  
ctccccggca ccagaagttc ctctgcgcgt ccgacggcga catgggcgtc 150  
cccacggccc tggaggccgg cagctggcgc tgggatccc tgctttcgc 200  
tctcttcctg gctgcgtccc taggtccgtt ggcagccttc aagggtcgcca 250  
cgccgtatttc cctgtatgtc tgtcccagg ggcagaacgt caccctcacc 300  
tgcaggctct tggccctgt ggacaaaggg cacgatgtga cttctacaa 350  
gacgtggta cgcagctcga gggcggaggt gcagacctgc tcagagcgcc 400  
ggcccatccg caacccacg ttccaggacc ttcacctgca ccatggaggc 450  
caccaggctg ccaacaccag ccacgacctg gtcagcgcc acgggctgga 500  
gtcggcctcc gaccaccatg gcaacttctc catcaccatg cgcaacctga 550  
ccctgctgga tagcggcctc tactgctgcc tgggtggta gatcaggcac 600  
caccactcgg agcacagggt ccatggtgcc atggagctgc aggtgcagac 650  
aggcaaagat gcaccatcca actgtgttgt gtaccatcc tcctccagg 700  
atagtgaaaa catcacggct gcagccctgg ctacgggtgc ctgcatacgta 750  
ggaatcctct gcctccccct catcctgctc ctggcttaca agcaaaggca 800  
ggcagcctcc aaccggcgtg cccaggagct ggtgcggatg gacagcaaca 850  
ttcaaggat tgaaaacccc ggctttaag ctcaccacc tgcccagggg 900  
atacccgagg ccaaagtca gcaaccctg tcctatgtgg cccagcggca 950  
gccttctgag tctggcggc atctgcttc ggagcccage acccccccgt 1000  
ctcctccagg ccccggagac gtcttcttcc catccctgga ccctgtccct 1050  
gactctccaa actttgaggt catctagccc agctggggga cagtggctg 1100  
ttgtggctgg gtctggggca ggtgcatttg agccaggagct ggctctgtga 1150  
gtggcctcct tggcctcggc cctgggttccc tccctcctgc tctgggctca 1200  
gatactgtga catcccagaa gcccagcccc tcaacccttc tggatgctac 1250  
atggggatgc tggacggctc agcccccgtt ccaaggattt tgggtgctg 1300  
agattctccc ctagagacct gaaattcacc agctacagat gccaaatgac 1350  
ttacatctta agaagtctca gaacgtccag cccttcagca gctctcggttc 1400  
tgagacatga gccttggat gtggcagcat cagtggaca agatggacac 1450

tgcccaccc tcccaggcac cagacacagg gcacgggtgga gagacttctc 1500  
ccccgtggcc gccttggctc ccccgttttgc cccgaggctg ctcttctgtc 1550  
agacttcctc tttgtaccac agtggctctg gggccaggcc tgcctgccc 1600  
ctggccatcg ccacccccc cagctgcctc ctaccagcag tttctctgaa 1650  
gatctgtcaa caggttaagt caatctgggg cttccactgc ctgcattcca 1700  
gtccccagag cttgggtggc ccgaaacggg aagtacatat tggggcatgg 1750  
tggcctccgt gagcaaatgg tgtcttggc aatctgaggc caggacagat 1800  
gttgccccac ccactggaga tggtgcttag ggaggtgggt ggggccttct 1850  
gggaaggtga gtggagaggg gcacctgccc cccgcccctcc ccatccccata 1900  
ctccccactgc tcagcgcggg ccattgcaag ggtgccacac aatgtcttgt 1950  
ccaccctggg acacttctga gtatgaagcg ggatgctatt aaaaactaca 2000  
tggggaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaga 2044

<210> 140  
<211> 311  
<212> PRT  
<213> Homo sapiens

<400> 140  
Met Gly Val Pro Thr Ala Leu Glu Ala Gly Ser Trp Arg Trp Gly  
1 5 10 15  
Ser Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Pro Val  
20 25 30  
Ala Ala Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro  
35 40 45  
Glu Gly Gln Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val  
50 55 60  
Asp Lys Gly His Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser  
65 70 75  
Ser Arg Gly Glu Val Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg  
80 85 90  
Asn Leu Thr Phe Gln Asp Leu His Leu His His Gly Gly His Gln  
95 100 105  
Ala Ala Asn Thr Ser His Asp Leu Ala Gln Arg His Gly Leu Glu  
110 115 120  
Ser Ala Ser Asp His His Gly Asn Phe Ser Ile Thr Met Arg Asn  
125 130 135  
Leu Thr Leu Leu Asp Ser Gly Leu Tyr Cys Cys Leu Val Val Glu

140	145	150
Ile Arg His His His Ser Glu His Arg Val His Gly Ala Met Glu		
155	160	165
Leu Gln Val Gln Thr Gly Lys Asp Ala Pro Ser Asn Cys Val Val		
170	175	180
Tyr Pro Ser Ser Ser Gln Asp Ser Glu Asn Ile Thr Ala Ala Ala		
185	190	195
Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys Leu Pro Leu		
200	205	210
Ile Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser Asn Arg		
215	220	225
Arg Ala Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile		
230	235	240
Glu Asn Pro Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro		
245	250	255
Glu Ala Lys Val Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln		
260	265	270
Pro Ser Glu Ser Gly Arg His Leu Leu Ser Glu Pro Ser Thr Pro		
275	280	285
Leu Ser Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp		
290	295	300
Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile		
305	310	

<210> 141  
<211> 1732  
<212> DNA  
<213> Homo sapiens

<400> 141  
cccacgcgtc cgcgcccttc ctttctgctg gacccctt cgtctctcca 50  
tctctccctc ctttccccgc gtctctttc caccttctc ttcttcccac 100  
cttagacctc ctttcctgcc ctcccttcct gccaccggct gtttcctggc 150  
ccttctccga ccccgctcta gcagcagacc tcctgggttc tgtgggttga 200  
tctgtggccc ctgtgcctcc gtgtcccttt cgtctccctt cttcccgact 250  
ccgctcccg accagcggcc tgaccctgg gaaaggatgg ttcccgaggt 300  
gagggtcctc tcctccttgc tgggactcgc gctgctctgg ttcccccctgg 350  
actcccacgc tcgagccgc ccagacatgt tctgccttt ccatggaaag 400  
agataactccc ccggcgagag ctggcacccc tacttgagc cacaaggcct 450

gatgtactgc ctgcgctgta cctgctcaga gggcgcccat gtgagttgtt 500  
accgcctcca ctgtccgcct gtccactgcc cccagcctgt gacggagcca 550  
cagcaatgct gtcccaagtg tgtggAACCT cacactccct ctggactccg 600  
ggccccacca aagtccctgcc agcacaacgg gaccatgtac caacacggag 650  
agatcttcag tgcccattgag ctgttccct cccgcctgcc caaccagtgt 700  
gtcctctgca gctgcacaga gggccagatc tactgcggcc tcacaacctg 750  
ccccgaacca ggctgcccag caccctccc actgccagac tcctgctgcc 800  
aagcctgcaa agatgaggca agtgagcaat cgatgaaaga ggacagtgtg 850  
cagtcgctcc atggggtgag acatcctcag gatccatgtt ccagtgtgc 900  
tgggagaaaag agaggcccgg gcaccccaagc ccccaactggc ctcagcgccc 950  
ctctgagctt catccctcgc cacttcagac ccaagggagc aggtagcaca 1000  
actgtcaaga tcgtcctgaa ggagaaacat aagaaagcct gtgtcatgg 1050  
cgggaaagacg tactcccacg gggaggtgtg gcacccggcc ttccgtgcct 1100  
tcggccctt gccctgcatt ctatgcaccc gtgaggatgg cccggaggac 1150  
tgccagcgtg tgacctgtcc caccgagtac ccctgcccgc accccgagaa 1200  
agtggctggg aagtgtcga agatggccca agaggacaaa gcagaccctg 1250  
gccacagtga gatcagttct accaggtgtc ccaagggacc gggccgggtc 1300  
ctcgtccaca catcggtatc cccaaagccca gacaacctgc gtcgtttgc 1350  
ccttggAACAC gaggcctcgg acttgggtgga gatctacctc tggaaagctgg 1400  
taaaagatga ggaaactgag gtcagagag gtgaagtacc tggcccaagg 1450  
ccacacagcc agaatcttcc acttgactca gatcaagaaa gtcaggaagc 1500  
aagacttcca gaaagaggca cagcacttcc gactgctcgc tggcccccac 1550  
gaaggtcact ggaacgtctt cctagcccaag accctggagc tgaaggtcac 1600  
ggccagtcca gacaaagtga ccaagacata acaaagacct aacagttgca 1650  
gatatgagct gtataattgt tgattattata tattaataaa taagaagttg 1700  
cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732  
<210> 142  
<211> 451  
<212> PRT  
<213> Homo sapiens  
<400> 142

Met Val Pro Glu Val Arg Val Leu Ser Ser Leu Leu Gly Leu Ala  
 1 5 10 15  
 Leu Leu Trp Phe Pro Leu Asp Ser His Ala Arg Ala Arg Pro Asp  
 20 25 30  
 Met Phe Cys Leu Phe His Gly Lys Arg Tyr Ser Pro Gly Glu Ser  
 35 40 45  
 Trp His Pro Tyr Leu Glu Pro Gln Gly Leu Met Tyr Cys Leu Arg  
 50 55 60  
 Cys Thr Cys Ser Glu Gly Ala His Val Ser Cys Tyr Arg Leu His  
 65 70 75  
 Cys Pro Pro Val His Cys Pro Gln Pro Val Thr Glu Pro Gln Gln  
 80 85 90  
 Cys Cys Pro Lys Cys Val Glu Pro His Thr Pro Ser Gly Leu Arg  
 95 100 105  
 Ala Pro Pro Lys Ser Cys Gln His Asn Gly Thr Met Tyr Gln His  
 110 115 120  
 Gly Glu Ile Phe Ser Ala His Glu Leu Phe Pro Ser Arg Leu Pro  
 125 130 135  
 Asn Gln Cys Val Leu Cys Ser Cys Thr Glu Gly Gln Ile Tyr Cys  
 140 145 150  
 Gly Leu Thr Thr Cys Pro Glu Pro Gly Cys Pro Ala Pro Leu Pro  
 155 160 165  
 Leu Pro Asp Ser Cys Cys Gln Ala Cys Lys Asp Glu Ala Ser Glu  
 170 175 180  
 Gln Ser Asp Glu Glu Asp Ser Val Gln Ser Leu His Gly Val Arg  
 185 190 195  
 His Pro Gln Asp Pro Cys Ser Ser Asp Ala Gly Arg Lys Arg Gly  
 200 205 210  
 Pro Gly Thr Pro Ala Pro Thr Gly Leu Ser Ala Pro Leu Ser Phe  
 215 220 225  
 Ile Pro Arg His Phe Arg Pro Lys Gly Ala Gly Ser Thr Thr Val  
 230 235 240  
 Lys Ile Val Leu Lys Glu Lys His Lys Lys Ala Cys Val His Gly  
 245 250 255  
 Gly Lys Thr Tyr Ser His Gly Glu Val Trp His Pro Ala Phe Arg  
 260 265 270  
 Ala Phe Gly Pro Leu Pro Cys Ile Leu Cys Thr Cys Glu Asp Gly  
 275 280 285  
 Arg Gln Asp Cys Gln Arg Val Thr Cys Pro Thr Glu Tyr Pro Cys

290	295	300
Arg His Pro Glu Lys Val Ala Gly Lys Cys Cys Lys Ile Cys Pro		
305	310	315
Glu Asp Lys Ala Asp Pro Gly His Ser Glu Ile Ser Ser Thr Arg		
320	325	330
Cys Pro Lys Ala Pro Gly Arg Val Leu Val His Thr Ser Val Ser		
335	340	345
Pro Ser Pro Asp Asn Leu Arg Arg Phe Ala Leu Glu His Glu Ala		
350	355	360
Ser Asp Leu Val Glu Ile Tyr Leu Trp Lys Leu Val Lys Asp Glu		
365	370	375
Glu Thr Glu Ala Gln Arg Gly Glu Val Pro Gly Pro Arg Pro His		
380	385	390
Ser Gln Asn Leu Pro Leu Asp Ser Asp Gln Glu Ser Gln Glu Ala		
395	400	405
Arg Leu Pro Glu Arg Gly Thr Ala Leu Pro Thr Ala Arg Trp Pro		
410	415	420
Pro Arg Arg Ser Leu Glu Arg Leu Pro Ser Pro Asp Pro Gly Ala		
425	430	435
Glu Gly His Gly Gln Ser Arg Gln Ser Asp Gln Asp Ile Thr Lys		
440	445	450

Thr

<210> 143  
<211> 693  
<212> DNA  
<213> Homo sapiens

<400> 143  
ctagcctgcg ccaagggtta gtgagaccgc gcggcaacag cttgcggctg 50  
cggggagctc ccgtgggcgc tccgctggct gtgcaggcg ccatggattc 100  
cttgcggaaa atgctgatct cagtcgcaat gctggcgca gggctggcg 150  
tgggctacgc gctcctcggtt atcgtgaccc cggagagcgc gcggaaagcag 200  
gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250  
ggccaggacc cagcagctat tgctggccac tctgcaggag gcagcgcacca 300  
cgcaggagaa cgtggcctgg aggaagaact ggatggttgg cggcgaaggc 350  
ggcgccagcg ggaggtcacc gtgagaccgg acttgctcc gtggcgccg 400  
gaccttggct tggcgcagg aatccgaggc agccttctc ctgcgtggc 450

ccagcggaga gtccggaccg agataccatg ccaggactct ccggggtcct 500  
gtgagctgcc gtcgggtgag cacgttccc ccaaaccctg gactgactgc 550  
tttaaggtcc gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600  
aactgaaaga accaataaaa tcatgttcct ccaaaaaaaaaaaaaaaa 650  
aaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaa 693

<210> 144  
<211> 93  
<212> PRT  
<213> Homo sapiens

<400> 144  
Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly  
1 5 10 15  
Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro  
20 25 30  
Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln  
35 40 45  
Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu  
50 55 60  
Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala  
65 70 75  
Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Ala Ser Gly  
80 85 90  
Arg Ser Pro

<210> 145  
<211> 1883  
<212> DNA  
<213> Homo sapiens

<400> 145  
caggagagaa ggcaccgccc ccaccccgcc tccaaagcta accctcggtc 50  
ttgagggaa gaggctgact gtacgttcct tctactctgg caccactctc 100  
caggctgcca tggggcccaag caccctctc ctcatctgt tcctttgtc 150  
atggtcggga cccctccaag gacagcagca ccaccttgtg gagtacatgg 200  
aacgcccact agctgcttta gaggaacggc tggccctgtg ccaggaccag 250  
agtagtcggc atgctgctga gctgcgggac ttcaagaaca agatgctgcc 300  
actgctggag gtggcagaga aggagcggga ggcactcaga actgaggccg 350  
acaccatctc cgggagagtg gatcgtctgg agcgggaggt agactatctg 400

gagacccaga acccagctct gccctgtgta gagtttgatg agaagggtac 450  
tggaggccct gggaccaaag gcaagggaag aaggaatgag aagtacgata 500  
tgggtgacaga ctgtggctac acaatcttc aagtggatc aatgaagatt 550  
ctgaagcgat ttgggtggccc agctggctta tggaccaagg atccactggg 600  
gcaaacagag aagatctacg tgtagatgg gacacagaat gacacagcct 650  
ttgtcttccc aaggctgcgt gacttcaccc ttgccatggc tgcccgaaa 700  
gcttcccggag tccgggtgcc cttccctgg gttaggcacag ggcagctgg 750  
atatggtggc tttctttatt ttgctcggag gcctcctgga agacctggtg 800  
gaggtggtga gatggagaac actttgcagc taatcaaatt ccacctggca 850  
aaccgaacag tgggtggacag ctcagtattc ccagcagagg ggctgatccc 900  
cccctacggc ttgacagcag acacctacat cgacctggta gctgatgagg 950  
aaggctttg ggctgtctat gccacccggg aggatgacag gcacttgg 1000  
ctggccaagt tagatccaca gacactggac acagagcagc agtgggacac 1050  
accatgtccc agagagaatg ctgaggctgc cttgtcatc tgtgggaccc 1100  
tctatgtcgt ctataacacc cgtcctgcca gtcggggccg catccagtgc 1150  
tcctttgatg ccagcggcac cctgacccct gaacgggcag cactcccta 1200  
ttttccccgc agatatggtg cccatgccag cctccgctat aaccccccgg 1250  
aacggccagct ctatgcctgg gatgatggct accagattgt ctataagctg 1300  
gagatgagga agaaagagga ggagggttga ggagctagcc ttgtttttg 1350  
catctttctc actcccatac atttatatta tatccccact aaatttctg 1400  
ttcctcattc ttcaaatgtg ggccagttgt ggctcaaatc ctctatattt 1450  
ttagccaatg gcaatcaaat tcttcagct ctttggatc atacggaaact 1500  
ccagatcctg agtaatcctt ttagagcccg aagagtcaaa accctcaatg 1550  
ttccctcctg ctctcctgccc ccatgtcaac aaatttcagg ctaaggatgc 1600  
cccgagacca gggctctaac cttgtatgct ggcaggccca gggagcaggc 1650  
agcagtgttc ttcccctcag agtgacttgg ggagggagaa ataggaggag 1700  
acgtccagct ctgtcctctc ttcctcactc ctcccttcag tgtcctgagg 1750  
aacaggactt tctccacatt gtttggatc gcaacatggt gcattaaaaag 1800  
aaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850

aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaa 1883

<210> 146

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

Met Gly Pro Ser Thr Pro Leu Leu Ile Leu Phe Leu Leu Ser Trp  
1 5 10 15

Ser Gly Pro Leu Gln Gly Gln Gln His His Leu Val Glu Tyr Met  
20 25 30

Glu Arg Arg Leu Ala Ala Leu Glu Glu Arg Leu Ala Gln Cys Gln  
35 40 45

Asp Gln Ser Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn  
50 55 60

Lys Met Leu Pro Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala  
65 70 75

Leu Arg Thr Glu Ala Asp Thr Ile Ser Gly Arg Val Asp Arg Leu  
80 85 90

Glu Arg Glu Val Asp Tyr Leu Glu Thr Gln Asn Pro Ala Leu Pro  
95 100 105

Cys Val Glu Phe Asp Glu Lys Val Thr Gly Gly Pro Gly Thr Lys  
110 115 120

Gly Lys Gly Arg Arg Asn Glu Lys Tyr Asp Met Val Thr Asp Cys  
125 130 135

Gly Tyr Thr Ile Ser Gln Val Arg Ser Met Lys Ile Leu Lys Arg  
140 145 150

Phe Gly Gly Pro Ala Gly Leu Trp Thr Lys Asp Pro Leu Gly Gln  
155 160 165

Thr Glu Lys Ile Tyr Val Leu Asp Gly Thr Gln Asn Asp Thr Ala  
170 175 180

Phe Val Phe Pro Arg Leu Arg Asp Phe Thr Leu Ala Met Ala Ala  
185 190 195

Arg Lys Ala Ser Arg Val Arg Val Pro Phe Pro Trp Val Gly Thr  
200 205 210

Gly Gln Leu Val Tyr Gly Gly Phe Leu Tyr Phe Ala Arg Arg Pro  
215 220 225

Pro Gly Arg Pro Gly Gly Gly Glu Met Glu Asn Thr Leu Gln  
230 235 240

Leu Ile Lys Phe His Leu Ala Asn Arg Thr Val Val Asp Ser Ser  
245 250 255

Val Phe Pro Ala Glu Gly Leu Ile Pro Pro Tyr Gly Leu Thr Ala  
 260 265 270  
 Asp Thr Tyr Ile Asp Leu Val Ala Asp Glu Glu Gly Leu Trp Ala  
 275 280 285  
 Val Tyr Ala Thr Arg Glu Asp Asp Arg His Leu Cys Leu Ala Lys  
 290 295 300  
 Leu Asp Pro Gln Thr Leu Asp Thr Glu Gln Gln Trp Asp Thr Pro  
 305 310 315  
 Cys Pro Arg Glu Asn Ala Glu Ala Ala Phe Val Ile Cys Gly Thr  
 320 325 330  
 Leu Tyr Val Val Tyr Asn Thr Arg Pro Ala Ser Arg Ala Arg Ile  
 335 340 345  
 Gln Cys Ser Phe Asp Ala Ser Gly Thr Leu Thr Pro Glu Arg Ala  
 350 355 360  
 Ala Leu Pro Tyr Phe Pro Arg Arg Tyr Gly Ala His Ala Ser Leu  
 365 370 375  
 Arg Tyr Asn Pro Arg Glu Arg Gln Leu Tyr Ala Trp Asp Asp Gly  
 380 385 390  
 Tyr Gln Ile Val Tyr Lys Leu Glu Met Arg Lys Lys Glu Glu Glu  
 395 400 405  
 Val

<210> 147  
 <211> 2052  
 <212> DNA  
 <213> Homo sapiens

<400> 147  
 gacagctgtg tctcgatgga gtagactctc agaacagcgc agtttgcct 50  
 ccgctcacgc agagcctctc cgtggcttcc gcacccgttgc cattaggcca 100  
 gttctcctct tctctcta at ccatccgtca cctctcctgt catccgttcc 150  
 catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200  
 ttggttctga gtctcccaa gctgggatca gggcagtggc aggtgtttgg 250  
 gccagacaag cctgtccagg ccttgggggg ggaggacgca gcattctcct 300  
 gtttcctgtc tcctaagacc aatgcagagg ccatggaagt gcggttcttc 350  
 aggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400  
 gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtaagg 450  
 attctattgc ggaggggcgc atctctctga ggctgaaaa cattactgtg 500

ttggatgctg gcctctatgg gtgcaggatt agttccagt cttactacca 550  
gaaggccatc tgggagctac aggtgtcagc actgggctca gttcctctca 600  
tttccatcac gggatatgtt gatagagaca tccagctact ctgtcagtc 650  
tcgggctgg tccccggcc cacagcgaag tggaaaggc cacaaggaca 700  
ggatttgtcc acagactcca ggacaaacag agacatgcat ggcctgttg 750  
atgtggagat ctctctgacc gtccaagaga acgcgggag catatcctgt 800  
tccatgcggc atgctcatct gagccgagag gtggaatcca gggtacagat 850  
aggagatacc ttttcgagc ctatatcgta gcacctggct accaaagtac 900  
tgggaataact ctgctgtggc ctatttttg gcattgttg actgaagatt 950  
ttcttctcca aattccagtg gaaaatccag gcggaaactgg actggagaag 1000  
aaagcacgga caggcagaat tgagagacgc ccggaaacac gcagtggagg 1050  
tgactctgga tccagagacg gtcacccga agctctgcgt ttctgatctg 1100  
aaaactgtaa cccatagaaa agctccccag gaggtgcctc actctgagaa 1150  
gagatttaca aggaagagtg tggtgcttc tcagagttc caagcaggga 1200  
aacattactg ggaggtggac ggaggacaca ataaaaaggtg gcgcgtggga 1250  
gtgtgccggg atgatgtgga caggaggaag gagtacgtga ctttgtctcc 1300  
cgatcatggg tactgggtcc tcagactgaa tggagaacat ttgtatttca 1350  
cattaaatcc ccgttttatac agcgtttcc ccaggacccc acctacaaaa 1400  
atagggtct tcctggacta tgagtgtggg accatctcct tcttcaacat 1450  
aaatgaccag tcccttattt ataccctgac atgtcggttt gaaggcttat 1500  
tgaggcccta cattgagttt ccgtcctata atgagcaaaa tggaaactccc 1550  
atagtcatct gcccagtcac ccaggaatca gagaaagagg cctcttggca 1600  
aagggcctct gcaatccca agacaagcaa cagttagtcc tcctcacagg 1650  
caaccacgccc cttccctcccc aggggtgaaa tgttaggatga atcacatccc 1700  
acattcttct ttagggatataa taaggctct ctcccaagatc caaagtcccg 1750  
cagcagccgg ccaagggtggc ttccagatga agggggactg gcctgtccac 1800  
atgggagtcg ggtgtcatgg ctgcccgttag ctggggaggga agaaggctga 1850  
cattacattt agtttgctct cactccatct ggctaagtga tcttgaataa 1900  
ccacctctca ggtgaagaac cgtaggaat tcccatctca caggctgtgg 1950

ttagattaa gtagacaagg aatgtgaata atgcttagat cttattgtat 2000  
 acagagtgtt tcctaattgtt ttgttcattt tattacactt tcagtaaaaa 2050  
 aa 2052

<210> 148  
 <211> 500  
 <212> PRT  
 <213> Homo sapiens

<400> 148  
 Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly  
 1 5 10 15

Ser Gly Gln Trp Gln Val Phe Gly Pro Asp Lys Pro Val Gln Ala  
 20 25 30

Leu Val Gly Glu Asp Ala Ala Phe Ser Cys Phe Leu Ser Pro Lys  
 35 40 45

Thr Asn Ala Glu Ala Met Glu Val Arg Phe Phe Arg Gly Gln Phe  
 50 55 60

Ser Ser Val Val His Leu Tyr Arg Asp Gly Lys Asp Gln Pro Phe  
 65 70 75

Met Gln Met Pro Gln Tyr Gln Gly Arg Thr Lys Leu Val Lys Asp  
 80 85 90

Ser Ile Ala Glu Gly Arg Ile Ser Leu Arg Leu Glu Asn Ile Thr  
 95 100 105

Val Leu Asp Ala Gly Leu Tyr Gly Cys Arg Ile Ser Ser Gln Ser  
 110 115 120

Tyr Tyr Gln Lys Ala Ile Trp Glu Leu Gln Val Ser Ala Leu Gly  
 125 130 135

Ser Val Pro Leu Ile Ser Ile Thr Gly Tyr Val Asp Arg Asp Ile  
 140 145 150

Gln Leu Leu Cys Gln Ser Ser Gly Trp Phe Pro Arg Pro Thr Ala  
 155 160 165

Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Thr Asp Ser Arg  
 170 175 180

Thr Asn Arg Asp Met His Gly Leu Phe Asp Val Glu Ile Ser Leu  
 185 190 195

Thr Val Gln Glu Asn Ala Gly Ser Ile Ser Cys Ser Met Arg His  
 200 205 210

Ala His Leu Ser Arg Glu Val Glu Ser Arg Val Gln Ile Gly Asp  
 215 220 225

Thr Phe Phe Glu Pro Ile Ser Trp His Leu Ala Thr Lys Val Leu

230	235	240
Gly Ile Leu Cys Cys Gly Leu Phe Phe	Gly Ile Val Gly Leu Lys	
245	250	255
Ile Phe Phe Ser Lys Phe Gln Trp Lys	Ile Gln Ala Glu Leu Asp	
260	265	270
Trp Arg Arg Lys His Gly Gln Ala Glu	Leu Arg Asp Ala Arg Lys	
275	280	285
His Ala Val Glu Val Thr Leu Asp Pro	Glu Thr Ala His Pro Lys	
290	295	300
Leu Cys Val Ser Asp Leu Lys Thr Val	Thr His Arg Lys Ala Pro	
305	310	315
Gln Glu Val Pro His Ser Glu Lys Arg	Phe Thr Arg Lys Ser Val	
320	325	330
Val Ala Ser Gln Ser Phe Gln Ala Gly	Lys His Tyr Trp Glu Val	
335	340	345
Asp Gly Gly His Asn Lys Arg Trp Arg	Val Gly Val Cys Arg Asp	
350	355	360
Asp Val Asp Arg Arg Lys Glu Tyr Val	Thr Leu Ser Pro Asp His	
365	370	375
Gly Tyr Trp Val Leu Arg Leu Asn Gly	Glu His Leu Tyr Phe Thr	
380	385	390
Leu Asn Pro Arg Phe Ile Ser Val Phe	Pro Arg Thr Pro Pro Thr	
395	400	405
Lys Ile Gly Val Phe Leu Asp Tyr Glu	Cys Gly Thr Ile Ser Phe	
410	415	420
Phe Asn Ile Asn Asp Gln Ser Leu Ile	Tyr Thr Leu Thr Cys Arg	
425	430	435
Phe Glu Gly Leu Leu Arg Pro Tyr Ile	Glu Tyr Pro Ser Tyr Asn	
440	445	450
Glu Gln Asn Gly Thr Pro Ile Val Ile	Cys Pro Val Thr Gln Glu	
455	460	465
Ser Glu Lys Glu Ala Ser Trp Gln Arg	Ala Ser Ala Ile Pro Glu	
470	475	480
Thr Ser Asn Ser Glu Ser Ser Ser Gln	Ala Thr Thr Pro Phe Leu	
485	490	495
Pro Arg Gly Glu Met		
500		

<210> 149  
<211> 24

<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 149  
gcgtggtcca cctctacagg gacg 24

<210> 150  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 150  
ggaactgacc cagtgctgac acc 23

<210> 151  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 151  
gcagatgcc a cgtatcaag gcaggacaaa actggtaag gattc 45

<210> 152  
<211> 2294  
<212> DNA  
<213> Homo sapiens

<400> 152  
gcgatggtgc gcccggtggc ggtggcgccg gcgggtgcgg aggcttcctt 50  
ggtcggattt caacgaggag aagatgactg accaaccgac tggctgaatg 100  
aatgaatggc ggagccgagc gcccattgag gagcctgccc agcctggcg 150  
gcctcgccct gtttgtctgc gcccggccg ccgcggccgt cgcctcagcc 200  
gcctcggcgg ggaatgtcac cggtggcgccg gggccggcg ggcaggtgga 250  
cgctcgccg ggccccgggt tgccggccgaa gcccagccac cccttcccta 300  
gggcgacggc tcccacggcc caggccccga ggaccggcc cccgcgcgcc 350  
accgtccacc gaccctggc tgcgacttct ccagccagt ccccgagac 400

caccctctt tggcgactg ctggaccctc ttccaccacc tttcaggcgc 450  
cgctcgcccc ctcgcccacc acccctccgg cgccggaacg cacttcgacc 500  
acctctcagg cgccgaccag acccgccgacc accaccctt cgacgaccac 550  
tggcccgccg ccgaccaccc ctgtagcgac caccgtaccg gcccacga 600  
ctccccggac cccgacccccc gatctccccca gcagcagcaa cagcagcgtc 650  
ctccccaccc cacctgccac cgaggccccc tcttcgcctc ctccagagta 700  
tgtatgtAAC tgctctgtgg ttggaaAGCCT gaatgtGAAT cgctgcaACC 750  
agaccacagg gcagtgtGAG tgcggccAG gttatcAGGG gcttcactGT 800  
gaaacctgca aagaggGCTT ttacctaAAT tacacttCTG ggctctgtCA 850  
gccatgtgac tgttagtCCAC atggagCTCT cagcatACCG tgcaacAGGT 900  
aagcaacaga gggTggAACT gaagtTTATT ttattttAGC aaggGaaaaAA 950  
aaaaggctgc tactctcaag gaccataCTG gtttaaACAA aggaggatGA 1000  
gggtcataga tttacaaaAT attttatATA cttttattCTC cttaCTttAT 1050  
atgttatatt taatgtcagg atttaAAAC atctaattTA ctgatTTAGt 1100  
tcttcaaaAG cactagAGTC gccaattttt ctctggata atttctgtAA 1150  
atttcatggg aaaaattat tgaagaataa atctgCTTC tggaggGCT 1200  
ttcaggcatg aaacctgcta ggaggTTAG aaatgttCTT atgtttATTa 1250  
atataccatt ggagTTGAG gaaatttGTT gtttggtta ttttctctc 1300  
taatcaaaAT tctacatttG tttctttGGA catctaaAGC ttaacctGGG 1350  
ggtaCCCTAA tttatTTAAC tagtggtaAG tagactggTT ttactctatt 1400  
taccagtaca ttttgagAC caaaAGTAGA ttaAGCAGGA attatCTTA 1450  
aactattatG ttatTTGGAG gtaatttaAT cttagtggAAAt aatgtactGT 1500  
tatctaAGCA tttgccttGT actgcactGA aagtaatttAT tcttgcACCT 1550  
tatgtgaggc acttggCTT ttgtggACCC caagtcaAAA aactgaAGAG 1600  
acagtattAA ataAtgAAAAA aaataatGAC aggttataCT cagtgtAAcc 1650  
tgggtataAC ccaagatCTG ctGCCACTTA cgagctgtGT tccttggca 1700  
agtaatttCC tttcactGAG ctgtttCTT ctcaaggTTG ttgtgaAGAT 1750  
taaatgagtt gatatatata aaatgcctAG cacatgtcac tcaataAAatt 1800  
ctggTTTgtt ttaatttCAA aggaatatta tggactgAAA tgagagaACA 1850

tgttttaaga acttttagct ccttgacaaa gaagtgcctt atacttttagc 1900  
actaaatatt ttaaatgctt tataaatgat attatactgt tatggaatat 1950  
tgtatcatat tgtagtttat taaaaatgta gaagaggctg ggcgcgggtgg 2000  
ctcacgcctg taatccttagc actttgggag gccaaaggcggtgg 2050  
tgagggccagg agttctagat gagcctggcc agcacagtga aaccccgctt 2100  
ctactaaaaa tacaaacaaa tttagctgggc gtgggtggcac acacctgttag 2150  
tccccagctac tcgggaggct gaggcaggag aatcggttga acccgggagg 2200  
tggaggttgc agtgagctga gatcgccca ctgcactcca gcctggtgag 2250  
agagggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153  
<211> 258  
<212> PRT  
<213> *Homo sapiens*

<400> 153

Met	Arg	Ser	Leu	Pro	Ser	Leu	Gly	Gly	Leu	Ala	Leu	Leu	Cys	Cys
1				5					10				15	
Ala	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ser	Ala	Ala	Ser	Ala	Gly	Asn
						20			25				30	
Val	Thr	Gly	Gly	Gly	Gly	Ala	Ala	Gly	Gln	Val	Asp	Ala	Ser	Pro
						35			40				45	
Gly	Pro	Gly	Leu	Arg	Gly	Glu	Pro	Ser	His	Pro	Phe	Pro	Arg	Ala
				50					55				60	
Thr	Ala	Pro	Thr	Ala	Gln	Ala	Pro	Arg	Thr	Gly	Pro	Pro	Arg	Ala
				65					70				75	
Thr	Val	His	Arg	Pro	Leu	Ala	Ala	Thr	Ser	Pro	Ala	Gln	Ser	Pro
				80					85				90	
Glu	Thr	Thr	Pro	Leu	Trp	Ala	Thr	Ala	Gly	Pro	Ser	Ser	Thr	Thr
				95					100				105	
Phe	Gln	Ala	Pro	Leu	Gly	Pro	Ser	Pro	Thr	Thr	Pro	Pro	Ala	Ala
				110					115				120	
Glu	Arg	Thr	Ser	Thr	Thr	Ser	Gln	Ala	Pro	Thr	Arg	Pro	Ala	Pro
				125					130				135	
Thr	Thr	Leu	Ser	Thr	Thr	Thr	Gly	Pro	Ala	Pro	Thr	Thr	Pro	Val
				140					145				150	
Ala	Thr	Thr	Val	Pro	Ala	Pro	Thr	Thr	Pro	Arg	Thr	Pro	Thr	Pro
				155					160				165	
Asp	Leu	Pro	Ser	Ser	Ser	Asn	Ser	Ser	Val	Leu	Pro	Thr	Pro	Pro

170                    175                    180  
Ala Thr Glu Ala Pro Ser Ser Pro Pro Pro Glu Tyr Val Cys Asn  
185                    190                    195  
Cys Ser Val Val Gly Ser Leu Asn Val Asn Arg Cys Asn Gln Thr  
200                    205                    210  
Thr Gly Gln Cys Glu Cys Arg Pro Gly Tyr Gln Gly Leu His Cys  
215                    220                    225  
Glu Thr Cys Lys Glu Gly Phe Tyr Leu Asn Tyr Thr Ser Gly Leu  
230                    235                    240  
Cys Gln Pro Cys Asp Cys Ser Pro His Gly Ala Leu Ser Ile Pro  
245                    250                    255  
Cys Asn Arg

<210> 154

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 154

aactgctctg tggtttggaaag cctg 24

<210> 155

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 155

cagtcacatg gctgacacagac ccac 24

<210> 156

<211> 38

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-38

<223> Synthetic construct.

<400> 156

aggatatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157  
<211> 689  
<212> DNA  
<213> Homo sapiens

<400> 157  
tgcggcgcag tgtagacctg ggaggatggg cggcctgctg ctggctgctt 50  
ttctggctt ggtctcggtg cccagggccc aggccgtgtg gttggaaaga 100  
ctggaccctg agcagcttct tggccctgg tacgtgcttgcggccctc 150  
ccggaaaaag ggcttgcca tggagaagga catgaagaac gtcgtggggg 200  
tggtggtgac cctcactcca gaaaacaacc tgccgacgct gtcctctcag 250  
cacgggctgg gagggtgtga ccagagtgtc atggacctga taaagcgaaa 300  
ctccggatgg gtgttgaga atccctcaat aggctgtgtc gagctctggg 350  
tgctggccac caacttcaga gactatgccatcatcttac tcagctggag 400  
ttcggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450  
agccagccag gaggccatgg ggctttcac caagtggagc aggagcctgg 500  
gcttcctgtc acagtagcag gcccagctgc agaaggacct cacctgtgtc 550  
cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcccccaca 600  
gggtcctgtg acctcgccatgttccaccc acctcgctca gcggctcccg 650  
gggcccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158  
<211> 163  
<212> PRT  
<213> Homo sapiens

<400> 158  
Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val  
1 5 10 15  
Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln  
20 25 30  
Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys  
35 40 45  
Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val  
50 55 60  
Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln  
65 70 75  
His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys  
80 85 90

Arg Asn Ser Gly Trp Val Phe Glu Asn Pro Ser Ile Gly Val Leu  
95 100 105

Glu Leu Trp Val Leu Ala Thr Asn Phe Arg Asp Tyr Ala Ile Ile  
110 115 120

Phe Thr Gln Leu Glu Phe Gly Asp Glu Pro Phe Asn Thr Val Glu  
125 130 135

Leu Tyr Ser Leu Thr Glu Thr Ala Ser Gln Glu Ala Met Gly Leu  
140 145 150

Phe Thr Lys Trp Ser Arg Ser Leu Gly Phe Leu Ser Gln  
155 160

<210> 159  
<211> 1665  
<212> DNA  
<213> Homo sapiens

<400> 159  
aacagacgtt ccctcgccgc cctggcacct ctaaccccaag acatgctgct 50  
gctgctgctg cccctgctct gggggaggga gagggcggaa ggacagacaa 100  
gtaaactgct gacgatgcag agttccgtga cggtgcagga aggccctgtgt 150  
gtccatgtgc cctgctcctt ctccatcccc tcgcatggct ggatttaccc 200  
tggcccagta gttcatggct actgggttccg ggaaggggcc aatacagacc 250  
aggatgctcc agtggccaca aacaacccaa ctcggcagt gtgggaggag 300  
actcgggacc gattccaccc cttggggac ccacatacca agaattgcac 350  
cctgagcatc agagatgccca gaagaagtga tgcggggaga tacttcttc 400  
gtatggagaa aggaagtata aaatggaatt ataaacatca ccggctctct 450  
gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500  
cctggagtcc ggctgcccc agaatctgac ctgctctgtg ccctgggcct 550  
gtgagcagg gacacccct atgatctcct ggataggac ctccgtgtcc 600  
ccccctggacc cctccaccac ccgctcctcg gtgctcaccc tcatacccaca 650  
gccccaggac catggcacca gcctcacctg tcaggtgacc ttcccgggg 700  
ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctacccgcct 750  
cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800  
cttggaaaat ggctcatctc tgtcaactccc agagggccag tctctgcgcc 850  
tggctgtgc agttgatgca gttgacagca atccccctgc caggctgagc 900  
ctgagctgga gaggcctgac cctgtcccc tcacagccct caaaccggg 950

ggtgctggag ctgccttggg tgcacctgag ggatgcagct gaattcacct 1000  
gcagagctca gaaccctctc ggctctcagc aggtctacct gaacgtctcc 1050  
ctgcagagca aagccacatc aggagtact caggggtgg tcgggggagc 1100  
tggagccaca gccctggtct tcctgtcctt ctgcgtcatc ttcggttag 1150  
ttaggtcctg caggaagaaa tcggcaaggc cagcagcggg cgtgggagat 1200  
acgggcatacg agatgcaaa cgctgtcagg gtttcagcct ctcaggggcc 1250  
cctgactgaa ccttgggcag aagacagtcc cccagaccag cctccccag 1300  
cttctgcccgc ctccctcagtg ggggaaggag agctccagta tgcatccctc 1350  
agcttccaga tggtaagcc ttgggactcg cgggacagg aggccactga 1400  
caccgagtac tcggagatca agatccacag atgagaaact gcagagactc 1450  
accctgatttgggatcaca gcccctccag gcaagggaga agtcagaggc 1500  
tgattcttgt agaattaaca gccctaactg tgatgagcta tgataacact 1550  
atgaattatg tgcagagtga aaagcacaca ggcttagag tcaaagtatc 1600  
tcaaacctga atccacactg tgccctccct tttttttt taactaaaag 1650  
acagacaaat tccta 1665

<210> 160  
<211> 463  
<212> PRT  
<213> Homo sapiens

<400> 160  
Met Leu Leu Leu Leu Pro Leu Leu Trp Gly Arg Glu Arg Ala  
1 5 10 15  
Glu Gly Gln Thr Ser Lys Leu Leu Thr Met Gln Ser Ser Val Thr  
20 25 30  
Val Gln Glu Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr  
35 40 45  
Pro Ser His Gly Trp Ile Tyr Pro Gly Pro Val Val His Gly Tyr  
50 55 60  
Trp Phe Arg Glu Gly Ala Asn Thr Asp Gln Asp Ala Pro Val Ala  
65 70 75  
Thr Asn Asn Pro Ala Arg Ala Val Trp Glu Glu Thr Arg Asp Arg  
80 85 90  
Phe His Leu Leu Gly Asp Pro His Thr Lys Asn Cys Thr Leu Ser  
95 100 105  
Ile Arg Asp Ala Arg Arg Ser Asp Ala Gly Arg Tyr Phe Phe Arg

110	115	120
Met Glu Lys Gly Ser Ile Lys Trp Asn Tyr Lys His His Arg Leu		
125	130	135
Ser Val Asn Val Thr Ala Leu Thr His Arg Pro Asn Ile Leu Ile		
140	145	150
Pro Gly Thr Leu Glu Ser Gly Cys Pro Gln Asn Leu Thr Cys Ser		
155	160	165
Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met Ile Ser Trp		
170	175	180
Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr Arg Ser		
185	190	195
Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr Ser		
200	205	210
Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn		
215	220	225
Lys Thr Val His Leu Asn Val Ser Tyr Pro Pro Gln Asn Leu Thr		
230	235	240
Met Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly		
245	250	255
Asn Gly Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu		
260	265	270
Val Cys Ala Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu		
275	280	285
Ser Leu Ser Trp Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser		
290	295	300
Asn Pro Gly Val Leu Glu Leu Pro Trp Val His Leu Arg Asp Ala		
305	310	315
Ala Glu Phe Thr Cys Arg Ala Gln Asn Pro Leu Gly Ser Gln Gln		
320	325	330
Val Tyr Leu Asn Val Ser Leu Gln Ser Lys Ala Thr Ser Gly Val		
335	340	345
Thr Gln Gly Val Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe		
350	355	360
Leu Ser Phe Cys Val Ile Phe Val Val Val Arg Ser Cys Arg Lys		
365	370	375
Lys Ser Ala Arg Pro Ala Ala Gly Val Gly Asp Thr Gly Ile Glu		
380	385	390
Asp Ala Asn Ala Val Arg Gly Ser Ala Ser Gln Gly Pro Leu Thr		
395	400	405

Glu Pro Trp Ala Glu Asp Ser Pro Pro Asp Gln Pro Pro Pro Ala  
410 415 420  
Ser Ala Arg Ser Ser Val Gly Glu Gly Glu Leu Gln Tyr Ala Ser  
425 430 435  
Leu Ser Phe Gln Met Val Lys Pro Trp Asp Ser Arg Gly Gln Glu  
440 445 450  
Ala Thr Asp Thr Glu Tyr Ser Glu Ile Lys Ile His Arg  
455 460

<210> 161  
<211> 739  
<212> DNA  
<213> Homo sapiens

<400> 161  
gacgcccagt gacctgccga ggtcgccagc acagagctct ggagatgaag 50  
accctgttcc tgggtgtcac gctcgccctg gccgctgccc tgtccttcac 100  
cctggaggag gaggatatac cagggacctg gtacgtgaag gccatggtgg 150  
tcgataagga ctttccggag gacaggaggc ccaggaaggt gtccccagtg 200  
aaggtgacag ccctggcgg tggaagttt gaagccacgt tcaccttcat 250  
gagggaggat cggtgcattcc agaagaaaat cctgatgcgg aagacggagg 300  
agcctggcaa atacagcgcc tatggggca ggaagctcat gtacctgcag 350  
gagctgccccaa ggagggacca ctacatctt tactgcaaag accagcacca 400  
tggggcctg ctccacatgg gaaagcttg ggttaggaat tctgataccca 450  
accgggaggc cctggaagaa tttaagaaat tggtgcaagc caagggactc 500  
tcggaggagg acatttcac gcccctgcag acgggaagct gcgttcccgaa 550  
acactaggca gccccgggt ctgcacccctt agagcccacc ctaccaccag 600  
acacagagcc cggaccaccc ggacctaccc tccagccatg acccttccct 650  
gctcccaccc acctgactcc aaataaaagtc cttttcccc aaaaaaaaaa 700  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162  
<211> 170  
<212> PRT  
<213> Homo sapiens

<400> 162  
Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala  
1 5 10 15  
Leu Ser Phe Thr Leu Glu Glu Asp Ile Thr Gly Thr Trp Tyr